OM protein - protein search, using sw model

Run on: March 7, 2006, 23:30:34 ; Search time 17.6033 Seconds
(without alignments)
1864.554 Million cell updates/sec

Title: US-10-621-855-5
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLLMILLLVLS.....PRLPILSFSILPLILLQTLW 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2131	100.0	397	2	US-09-220-528-64	Sequence 64, Appl
2	2131	100.0	397	2	US-09-187-906-17	Sequence 17, Appl
3	2131	100.0	397	2	US-09-489-407-17	Sequence 17, Appl
4	1774	83.2	346	2	US-09-187-906-15	Sequence 15, Appl
5	1774	83.2	346	2	US-09-489-407-15	Sequence 15, Appl
6	1646.5	77.3	400	2	US-09-220-528-63	Sequence 63, Appl
7	1646.5	77.3	400	2	US-09-187-906-21	Sequence 21, Appl
8	1646.5	77.3	400	2	US-09-949-016-9079	Sequence 9079, Ap
9	1646.5	77.3	400	2	US-09-489-407-21	Sequence 21, Appl
10	1386	65.0	315	2	US-09-187-906-19	Sequence 19, Appl
11	1386	65.0	315	2	US-09-489-407-19	Sequence 19, Appl
12	577.5	27.1	445	2	US-08-861-990-11	Sequence 11, Appl
13	577.5	27.1	464	2	US-08-957-063-6	Sequence 6, Appli
14	577.5	27.1	464	2	US-09-487-685-6	Sequence 6, Appli
15	577.5	27.1	464	2	US-08-802-805D-6	Sequence 6, Appli
16	577.5	27.1	464	2	US-08-861-990-2	Sequence 2, Appli
17	577.5	27.1	464	2	US-09-388-316C-6	Sequence 6, Appli
18	577.5	27.1	664	2	US-08-957-063-18	Sequence 18, Appl
19	577.5	27.1	664	2	US-09-487-685-18	Sequence 18, Appl
20	577.5	27.1	664	2	US-08-802-805D-18	Sequence 18, Appl
21	577.5	27.1	664	2	US-09-388-316C-18	Sequence 18, Appl
22	574.5	27.0	464	2	US-08-957-063-3	Sequence 3, Appli
23	574.5	27.0	464	2	US-09-487-685-3	Sequence 3, Appli
24	574.5	27.0	464	2	US-08-802-805D-3	Sequence 3, Appli
25	574.5	27.0	464	2	US-09-187-906-13	Sequence 13, Appl
26	574.5	27.0	464	2	US-08-861-990-9	Sequence 9, Appli
27	574.5	27.0	464	2	US-09-388-316C-3	Sequence 3, Appli
28	574.5	27.0	464	2	US-09-489-407-13	Sequence 13, Appl
29	574.5	27.0	664	2	US-08-957-063-16	Sequence 16, Appl
30	574.5	27.0	664	2	US-09-487-685-16	Sequence 16, Appl
31	574.5	27.0	664	2	US-08-802-805D-16	Sequence 16, Appl
32	574.5	27.0	664	2	US-09-388-316C-16	Sequence 16, Appl
33	515	24.2	460	2	US-08-802-805D-22	Sequence 22, Appl
34	515	24.2	460	2	US-09-187-906-11	Sequence 11, Appl
35	515	24.2	460	2	US-09-489-407-11	Sequence 11, Appl
36	513.5	24.1	463	2	US-08-837-199A-10	Sequence 10, Appl
37	513.5	24.1	463	2	US-08-837-199A-12	Sequence 12, Appl
38	513.5	24.1	465	2	US-08-837-199A-2	Sequence 2, Appli
39	513.5	24.1	465	2	US-08-861-990-8	Sequence 8, Appli
40	513.5	24.1	465	2	US-09-388-316C-22	Sequence 22, Appl
41	512.5	24.0	465	2	US-08-837-199A-6	Sequence 6, Appli
42	505.5	23.7	468	2	US-08-802-805D-21	Sequence 21, Appl
43	505.5	23.7	468	2	US-08-837-199A-4	Sequence 4, Appli
44	505.5	23.7	468	2	US-08-860-370-2	Sequence 2, Appli
45	505.5	23.7	468	2	US-09-187-906-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-220-528-64
; Sequence 64, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
; FILE REFERENCE: 6029-7998
; CURRENT APPLICATION NUMBER: US/09/220,528A
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Murine
US-09-220-528-64

Query Match 100.0%; Score 2131; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.2e-211;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
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Db         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
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Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
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Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
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Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
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RESULT 2
US-09-187-906-17
; Sequence 17, Application US/09187906
; Patent No. 6677135
; GENERAL INFORMATION:
;   APPLICANT:  BIOGEN, INC.
;   TITLE OF INVENTION:  Ret Ligand (RetL) for Stimulating Neural
;   TITLE OF INVENTION:  and Renal Growth
;   NUMBER OF SEQUENCES:  21
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Biogen, Inc.
;     STREET:  14 Cambridge Center
;     CITY:  Cambridge
;     STATE:  MA
;     COUNTRY:  USA
;     ZIP:  02142
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/187,906
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US97/07726
;     FILING DATE:  07-MAY-97
;     APPLICATION NUMBER:  US 60/017,427
;     FILING DATE:  08-MAY-96
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 60/019,300
;     FILING DATE:  07-JUN-96
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 60/021,859
;     FILING DATE:  16-JUL-96
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 60/043,533
;     FILING DATE:  10-APR-97
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Kaplan, Warren A.
;     REGISTRATION NUMBER:  34,199
;     REFERENCE/DOCKET NUMBER:  A008 PCT CIP
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  617-679-2400
;     TELEFAX:  617-679-2838
; INFORMATION FOR SEQ ID NO:  17:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  397 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-09-187-906-17

  Query Match             100.0%;  Score 2131;  DB 2;  Length 397;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-211;
  Matches  397;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
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Db          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
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Db         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
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Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
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Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
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Db        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300

Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
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RESULT 3
US-09-489-407-17
; Sequence 17, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
;   APPLICANT:  BIOGEN, INC.
;   TITLE OF INVENTION:  Ret Ligand (RetL) for Stimulating Neural
;   TITLE OF INVENTION:  and Renal Growth
;   NUMBER OF SEQUENCES:  21
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Biogen, Inc.
;     STREET:  14 Cambridge Center
;     CITY:  Cambridge
;     STATE:  MA
;     COUNTRY:  USA
;     ZIP:  02142
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/489,407
;     FILING DATE:
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US97/07726
;     FILING DATE:  07-MAY-97
;     APPLICATION NUMBER:  US 60/017,427
;     FILING DATE:  08-MAY-96
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 60/019,300
;     FILING DATE:  07-JUN-96
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 60/021,859
;     FILING DATE:  16-JUL-96
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 60/043,533
;     FILING DATE:  10-APR-97
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Kaplan, Warren A.
;     REGISTRATION NUMBER:  34,199
;     REFERENCE/DOCKET NUMBER:  A008 PCT CIP
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  617-679-2400
;     TELEFAX:  617-679-2838
; INFORMATION FOR SEQ ID NO:  17:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  397 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
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;    MOLECULE TYPE:  protein
US-09-489-407-17

  Query Match           100.0%;  Score 2131;  DB 2;  Length 397;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-211;
  Matches  397;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
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Db          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
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Db         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
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Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
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Db        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240

Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
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Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
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Db        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
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Db        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397


RESULT 4
US-09-187-906-15
; Sequence 15, Application US/09187906
; Patent No. 6677135
;  GENERAL INFORMATION:
;    APPLICANT:  BIOGEN, INC.
;    TITLE OF INVENTION:  Ret Ligand (RetL) for Stimulating Neural
;    TITLE OF INVENTION:  and Renal Growth
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Biogen, Inc.
;      STREET:  14 Cambridge Center
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02142
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/187,906
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US97/07726
;      FILING DATE:  07-MAY-97
;      APPLICATION NUMBER:  US 60/017,427
;      FILING DATE:  08-MAY-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/019,300
;      FILING DATE:  07-JUN-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/021,859
;      FILING DATE:  16-JUL-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/043,533
;      FILING DATE:  10-APR-97
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kaplan, Warren A.
;      REGISTRATION NUMBER:  34,199
;      REFERENCE/DOCKET NUMBER:  A008 PCT CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-679-2400
;      TELEFAX:  617-679-2838
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  346 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-187-906-15

  Query Match           83.2%;  Score 1774;  DB 2;  Length 346;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-174;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         68 LSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 127
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Db         17 LSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 76

Qy        128 LDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 LDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 136

Qy        188 CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 247
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Db        137 CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 196

Qy        248 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNT 307
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Qy        308 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQ 367
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Qy        368 QNSNPALRLQPRLPILSFSILPLILLQTLW 397
              ||||||||||||||||||||||||||||||
Db        317 QNSNPALRLQPRLPILSFSILPLILLQTLW 346


RESULT 5
US-09-489-407-15
; Sequence 15, Application US/09489407
; Patent No. 6861509
;  GENERAL INFORMATION:
;    APPLICANT:  BIOGEN, INC.
;    TITLE OF INVENTION:  Ret Ligand (RetL) for Stimulating Neural
;    TITLE OF INVENTION:  and Renal Growth
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Biogen, Inc.
;      STREET:  14 Cambridge Center
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02142
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/489,407
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US97/07726
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;      FILING DATE:  07-MAY-97
;      APPLICATION NUMBER:  US 60/017,427
;      FILING DATE:  08-MAY-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/019,300
;      FILING DATE:  07-JUN-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/021,859
;      FILING DATE:  16-JUL-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/043,533
;      FILING DATE:  10-APR-97
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kaplan, Warren A.
;      REGISTRATION NUMBER:  34,199
;      REFERENCE/DOCKET NUMBER:  A008 PCT CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-679-2400
;      TELEFAX:  617-679-2838
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  346 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-489-407-15

  Query Match             83.2%;  Score 1774;  DB 2;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-174;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         68 LSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 LSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 76

Qy        128 LDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 LDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 136

Qy        188 CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 196

Qy        248 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNT 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNT 256

Qy        308 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQ 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQ 316

Qy        368 QNSNPALRLQPRLPILSFSILPLILLQTLW 397
              ||||||||||||||||||||||||||||||
Db        317 QNSNPALRLQPRLPILSFSILPLILLQTLW 346


RESULT 6
US-09-220-528-63
; Sequence 63, Application US/09220528A
; Patent No. 6284540
; GENERAL INFORMATION:
;  APPLICANT: Milbrandt, Jeffrey D.
;  APPLICANT: Baloh, Robert H.
;  TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor
;  FILE REFERENCE: 6029-7998
;  CURRENT APPLICATION NUMBER: US/09/220,528A
;  CURRENT FILING DATE: 1998-12-24
;  EARLIER APPLICATION NUMBER: 09/218,698
;  EARLIER FILING DATE: 1998-12-22
;  EARLIER APPLICATION NUMBER: 60/108,148
;  EARLIER FILING DATE: 1998-11-12
;  EARLIER APPLICATION NUMBER: 09/163,283
;  EARLIER FILING DATE: 1998-09-29
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
;   LENGTH: 400
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-220-528-63

  Query Match             77.3%;  Score 1646.5;  DB 2;  Length 400;
  Best Local Similarity   77.8%;  Pred. No. 2.4e-161;
  Matches  305;  Conservative   30;  Mismatches   56;  Indels    1;  Gaps    1;

Qy          7 PRPP-LLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCT 65
              | || :||:|||:    ||| ||: | ||:| :||| |||:||:|:| | ||| || |||
Db          9 PLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRKCQADPTCSAAYHHLDSCT 68

Qy         66 SSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGD 125
              ||:| ||| || :: |||||||:|||||||| | |||||||:|  |||||||| |||||:
Db         69 SSISTPLPSEEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGN 128

Qy        126 YELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSG 185
              |||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        129 YELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLNDKCDRLRKAYGEACSG 188

Qy        186 IRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNC 245
              ||||:|| || :||||||| |||||||||||| | ||||||||||:|||| | |||
Db        189 PHCQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNC 248

Qy        246 LDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKV 305
              |:||  | :||||||||:|||||||||||||||||||||||||||||||||||:| |
Db        249 LELRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFVSNV 308

Qy        306 NTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVV 365
              ||:|||||||||||:||| ||  || |||| |||||||||| |||||||   ||:|:
Db        309 NTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMRFHSQLFSQDWPHPTFAVM 368

Qy        366 QQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
              || |||:| || :| |    |||||| :||
Db        369 AHQNENPAVRPQPWVPSLFSCTLPLILLLSLW 400


RESULT 7
US-09-187-906-21
; Sequence 21, Application US/09187906
; Patent No. 6677135
;  GENERAL INFORMATION:
;    APPLICANT:  BIOGEN, INC.
;    TITLE OF INVENTION:  Ret Ligand (RetL) for Stimulating Neural
;    TITLE OF INVENTION:  and Renal Growth
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Biogen, Inc.
;      STREET:  14 Cambridge Center
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02142
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/187,906
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US97/07726
;      FILING DATE:  07-MAY-97
;      APPLICATION NUMBER:  US 60/017,427
;      FILING DATE:  08-MAY-96
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/019,300
```

Hayes, R.
10/621855
Seq IDs 5 & 6

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 7, 2006, 23:29:17 ; Search time 67.6336 Seconds
(without alignments)
2579.093 Million cell updates/sec

Title: US-10-621-855-5
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLLMILLLVLS.....PRLPILSFSILPLILLQTLW 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2131	100.0	397	2	AAW37461	Aaw37461 Mouse Ret
2	2131	100.0	397	3	AAY84591	Aay84591 Amino aci
3	2131	100.0	397	3	AAY15174	Aay15174 Murine GF
4	2131	100.0	397	8	ADJ58709	Adj58709 Murine re
5	2131	100.0	397	9	ADY53845	Ady53845 Mouse ret
6	2131	100.0	397	9	ADZ00209	Adz00209 Mouse Ret
7	1972	92.5	397	2	AAW84182	Aaw84182 A GDNFR-a
8	1880	88.2	888	3	AAY15182	Aay15182 gD-GFRalp
9	1774	83.2	346	2	AAW37465	Aaw37465 Mouse Ret
10	1774	83.2	346	8	ADJ58707	Adj58707 Murine re
11	1774	83.2	346	9	ADY53843	Ady53843 Partial m
12	1774	83.2	346	9	ADZ00207	Adz00207 Mouse Ret
13	1646.5	77.3	400	2	AAW65116	Aaw65116 Human GDN
14	1646.5	77.3	400	2	AAW37463	Aaw37463 Human Ret
15	1646.5	77.3	400	2	AAW84186	Aaw84186 Glial cel
16	1646.5	77.3	400	3	AAY83226	PRO538 Po
17	1646.5	77.3	400	3	AAY84590	Aay84590 Amino aci
18	1646.5	77.3	400	3	AAY15177	Aay15177 Human GFR
19	1646.5	77.3	400	3	AAB19582	Aab19582 Human PRO
20	1646.5	77.3	400	3	AAB24411	Aab24411 Human PRO
21	1646.5	77.3	400	3	AAB00171	Aab00171 PRO538 po
22	1646.5	77.3	400	3	AAB24050	Aab24050 Human PRO
23	1646.5	77.3	400	8	ADJ58713	Adj58713 Human ret
24	1646.5	77.3	400	8	ADT94302	Adt94302 Human PRO
25	1646.5	77.3	400	9	ADY53849	Ady53849 Human ret
26	1646.5	77.3	400	9	ADZ00213	Adz00213 Human Ret
27	1646.5	77.3	628	3	AAY15179	Aay15179 GFRalpha3
28	1642.5	77.1	400	2	AAW84180	Aaw84180 A GDNFR-a
29	1640.5	77.0	400	2	AAW65117	Aaw65117 Human GDN
30	1531.5	71.9	378	2	AAW84185	Aaw84185 Glial cel
31	1458	68.4	369	3	AAY15178	Aay15178 Human GFR
32	1458	68.4	369	3	AAB19583	Aab19583 Human PRO
33	1458	68.4	369	3	AAB24051	Aab24051 Human PRO
34	1413	66.3	366	9	AEA39229	Aea39229 GRAL-rela
35	1386	65.0	315	2	AAW37462	Aaw37462 Human Ret
36	1386	65.0	315	8	ADJ58711	Adj58711 Human ret
37	1386	65.0	315	9	ADY53847	Ady53847 Partial h
38	1386	65.0	315	9	ADZ00211	Adz00211 Human Ret
39	722	33.9	172	2	AAW65118	Aaw65118 Human GDN
40	654	30.7	498	2	AAW84183	Aaw84183 Consensus
41	640.5	30.1	489	2	AAW84298	Aaw84298 Consensus
42	577.5	27.1	460	2	AAW84181	Aaw84181 A GDNFR-a
43	577.5	27.1	464	2	AAW71602	Aaw71602 Rat neurt
44	577.5	27.1	464	2	AAW92299	Aaw92299 Rat GDNFR
45	577.5	27.1	464	3	AAY80122	Aay80122 Rat neurt

ALIGNMENTS

RESULT 1
AAW37461
ID AAW37461 standard; protein; 397 AA.
XX
AC AAW37461;
XX
DT 21-MAY-1998 (first entry)
XX
DE Mouse Ret ligand RetL3.
XX
KW Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury; neurodegeneration;
KW motor neurone disease; multiple sclerosis; infection; meningitis;
KW myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury;
KW spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease;
KW muscular dystrophy; myasthenia gravis; tumour; therapy.
XX
OS Mus musculus.
XX
PN WO9744356-A2.
XX
PD 27-NOV-1997.
XX
PF 07-MAY-1997; 97WO-US007726.
XX
PR 08-MAY-1996; 96US-0017427P.
PR 07-JUN-1996; 96US-0019300P.
PR 16-JUL-1996; 96US-0021859P.
PR 11-APR-1997; 97US-0043533P.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Sanicola-Nadel M, Hession C, Cate RL;
XX
DR WPI; 1998-018431/02.
DR N-PSDB; AAV00249.
XX
PT New nucleic acid encoding ret receptor ligands and related proteins -
PT vectors, transformed cells and antibodies, used for promoting cell growth
PT and improving survival of injured cells, especially renal or nerve cells.
XX
PS Claim 2; Page 77-78; 113pp; English.
XX
CC This amino acid sequence comprises mouse Ret ligand (RetL) RetL3, deduced
CC from cDNA clones (see AAV00249) isolated from an EST database and by
CC 5'RACE. Rat and human RetL1, human RetL2 and RetL3 sequences (see

CC AAW37457-60 and AAW37462-63) are also claimed. RetL is a key component of
CC the Ret signalling pathway that specifically interacts with Ret receptor
CC protein, triggering Ret dimerisation and/or autophosphorylation of the
CC Ret tyrosine kinase domain. Vectors containing retL3 DNA and prokaryotic
CC or eukaryotic host cells transformed or transfected with these vectors
CC are claimed, as well as a method for production of RetL3, its soluble
CC variants and fusion proteins with a toxin, imageable compound or
CC radionuclide. RetL3, optionally when expressed from vectors in vivo, is
CC used to promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in renal
CC failure, nephritis, kidney transplants, toxic or hypoxic injury,
CC neurodegeneration, motor neurone disease, multiple sclerosis, bacterial,
CC viral or prion infections (e.g. meningitis, myelopathy associated with
CC HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury,
CC developmental disorders such as Down's syndrome and cerebral palsy, or
CC conditions involving the peripheral nervous system (Lyme disease,
CC muscular dystrophy and myasthenia gravis). Fusion proteins are used to
CC deliver toxins etc. to Ret-expressing cells, especially tumours
XX
SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.5e-198;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240

Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300

Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
              |||||||||||||||||||||||||||||||||||||
Db        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
```

RESULT 2
AAY84591
ID AAY84591 standard; protein; 397 AA.
XX
AC AAY84591;
XX
DT 25-JUL-2000 (first entry)
XX
DE Amino acid sequence of a human growth factor receptor-alpha precursor.
XX
KW Human; artemin; growth factor; neurotrophic factor; trophic support;
KW neuron; trigeminal ganglion neuron; nodose ganglion neuron;
KW superior cervical ganglion neuron; midbrain neuron; Alzheimer's disease;
KW peripheral neuropathy; amylotrophic lateral sclerosis; ischemic stroke;
KW Parkinson's disease; Huntington's disease; acute brain injury;
KW acute spinal cord injury; nervous system tumour; blastoma;
KW multiple sclerosis; infection; enteric disease; idiopathic constipation;
KW Parkinson's disease; small cell lung carcinoma.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1. .28
FT /note= "signal peptide"
FT Protein 29. .369
FT /note= "mature protein"
FT Modified-site 92
FT /note= "putative N-linked glycosylation site"
FT Modified-site 145
FT /note= "putative N-linked glycosylation site"
FT Modified-site 306
FT /note= "putative N-linked glycosylation site"
XX
PN WO200018799-A1.
XX
PD 06-APR-2000.
XX
PF 29-SEP-1999; 99WO-US022604.
XX
PR 29-SEP-1998; 98US-00163283.
PR 12-NOV-1998; 98US-0108148P.
PR 22-DEC-1998; 98US-00218698.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Milbrandt JD, Baloh RH;
XX
DR WPI; 2000-293109/25.
XX
PT Isolated artemin growth factor proteins and the nucleic acids that encode
PT them, useful for treating a range of degenerative neuronal disorders such
PT as Parkinson's disease and Huntington's disease.
XX
PS Disclosure; Fig 12; 96pp; English.
XX
CC The present sequence represents a murine growth factor receptor-alpha
CC precursor. The specification describrs an artemin growth factor protein.
CC Artemin is a neurotrophic factor that belongs to the GDNF (glial cell
CC line-derived neurotrophic factor)/neurturin/persephin family of growth
CC factors and promotes differentiation, maintains mature phenotype and
CC provides trophic support, promoting growth and survival of neurons.
CC Artemin promotes the survival of trigeminal ganglion neurons, nodose
CC ganglion neurons, superior cervical ganglion neurons and tyrosine-
CC hydroxylase-expressing dopaminergic ventral midbrain neurons. Artemin is
CC the only member of the GDNF family that binds to GFR-alpha (growth factor
CC receptor-alpha) and activates the GFR-alpha3/RET (Ret protein- tyrosine
CC kinase) receptor complex and additionally, like GDNF and neurturin,
CC artemin also binds to and activates GFRalpha1/RET. Artemin polypeptides
CC and polynucleotides are administered to treat peripheral neuropathy,
CC amylotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease,
CC Huntington's disease, ischemic stroke, acute brain injury, acute spinal
CC cord injury, a nervous system tumour (e.g. blastomas), multiple
CC sclerosis, infection or enteric disease (e.g. idiopathic constipation or
CC constipation associated with Parkinson's disease, spinal cord injury or
CC use of opiate pain killers). They may also be used to treat a patient
CC suffering from small cell lung carcinoma
XX
SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 3; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.5e-198;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240

Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300

Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
                |||||||||||||||||||||||||||||||||||||
Db        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
```

```
RESULT 3
AAY15174
ID   AAY15174 standard; protein; 397 AA.
XX
AC   AAY15174;
XX
DT   07-FEB-2000  (first entry)
XX
DE   Murine GFRalpha3.
XX
KW   Murine GFRalpha3; GFRalpha3; GFRalpha1;
KW   glial-cell-line-derived neurotrophic factor family receptor alpha-3;
KW   probe; homologous DNA; neuronal cell activation; GFRalpha3 ligand;
KW   cell proliferation; cell differentiation; GFRalpha3-containing cell;
KW   Ret-containing cell; peripheral nervous system disease; diabetes;
KW   human immunodeficiency virus; chemotherapeutic agent treatment;
KW   autonomic nervous system dysfunction; transgenic animal.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .27
FT                   /label= Signal_peptide
FT   Modified-site   92. .95
FT                   /note= "Potential glycosylation site"
FT   Modified-site   145. .148
FT                   /note= "Potential glycosylation site"
FT   Region          392. .397
FT                   /note= "C-terminal hydrophobic sequence associated with
FT                   GPI-anchoring"
XX
PN   WO9949039-A2.
XX
PD   30-SEP-1999.
XX
PF   19-MAR-1999;   99WO-US006098.
XX
PR   23-MAR-1998;   98US-0079124P.
PR   13-APR-1998;   98US-0081569P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   De Sauvage FJ,  Klein RD,  Phillips HS,  Rosenthal A;
XX
DR   WPI; 2000-038358/03.
DR   N-PSDB; AAZ29100.
XX
PT   New isolated GFR-alpha3 nucleic acid, used to develop products for
PT   treating diseases or conditions involving peripheral nervous system or
PT   automic nervous system.
XX
PS   Example 1; Fig 1; 112pp; English.
XX
CC   The present sequence is the full length mouse glial-cell-line-derived
CC   neurotrophic factor family receptor alpha-3 (GFRalpha3). This has
CC   sequence identity with GFRalpha1. GFRalpha3 DNA or its fragments can be
CC   used as a probe to screen for homologous DNA. GFRalpha3 possess neuronal
CC   cell activation property. GFRalpha3 ligands can be used to stimulate
CC   proliferation, growth, survival, differentiation, metabolism or
CC   regeneration of GFRalpha3- and Ret-containing cells. They can be useful
CC   in the treatment of peripheral nervous system diseases, eg. those
CC   associated with diabetes, human immunodeficiency virus, or
CC   chemotherapeutic agent treatments. Agonist or antagonists of GFRalpha3
CC   can be used to treat autonomic nervous system dysfunctions. The products
CC   can also be used for detection, diagnosis and production of transgenic
CC   animals
XX
SQ   Sequence 397 AA;
```

```
  Query Match             100.0%;  Score 2131;  DB 3;  Length 397;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-198;
  Matches  397;  Conservative    0; -Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240

Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300

Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
              |||||||||||||||||||||||||||||||||||||
Db        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
```

```
RESULT 4
ADJ58709
ID   ADJ58709 standard; protein; 397 AA.
XX
AC   ADJ58709;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Murine retL3 protein.
XX
KW   Tissue growth; retL protein; organ failure; foetal malformation;
KW   tumour growth; renal tissue; cytostatic; vulnerary; nephrotropic; murine.
XX
OS   Mus sp.
XX
PN   US6677135-B1.
XX
PD   13-JAN-2004.
XX
PF   06-NOV-1998;   98US-00187906.
XX
PR   08-MAY-1996;   96US-0017427P.
PR   07-JUN-1996;   96US-0019300P.
PR   16-JUL-1996;   96US-0021859P.
```

PR 23-AUG-1996; 96US-0023444P.
PR 11-APR-1997; 97US-0043533P.
PR 07-MAY-1997; 97WO-US007726.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
XX
DR WPI; 2004-079845/08.
DR N-PSDB; ADJ58708.
XX
PT New nucleic acid encoding Ret polypeptide, useful for diagnosing and/or
PT treating diseases or conditions associated with aberrant expression or
PT activity of the Ret ligand, such as organ failure, fetal malformations
PT and tumor growth.
XX
PS Claim 1; SEQ ID NO 17; 66pp; English.
XX
CC The present invention relates to nucleotide and amino acid sequences
CC which promote tissue growth and methods for modulating tissue growth. The
CC invention also relates to retL proteins and polynucleotides encoding such
CC proteins. RetL proteins interact with a receptor protein Ret to trigger
CC dimerisation and/or autophosphorylation of the tyrosine kinase domain of
CC the receptor protein Ret. The methods and compositions of the present
CC invention are useful for the diagnosis and/or treatment of diseases or
CC conditions associated with aberrant expression or activity of the Ret
CC ligand, such as organ failure, foetal malformations and tumour growth and
CC for promoting regeneration or survival of damaged renal tissue. The
CC present sequence is murine retL3 protein of the invention.
XX
SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 8; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.5e-198;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240

Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300

Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
              |||||||||||||||||||||||||||||||||||||
Db        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
```

RESULT 5
ADY53845
ID ADY53845 standard; protein; 397 AA.
XX
AC ADY53845;
XX
DT 05-MAY-2005 (first entry)
XX
DE Mouse retL3 protein.
XX
KW DNA purification; immune stimulation; ret ligand.
XX
OS Mus sp.
XX
PN US6861509-B1.
XX
PD 01-MAR-2005.
XX
PF 21-JAN-2000; 2000US-00489407.
XX
PR 08-MAY-1996; 96US-0017427P.
PR 07-JUN-1996; 96US-0019300P.
PR 16-JUL-1996; 96US-0021859P.
PR 23-AUG-1996; 96US-0023444P.
PR 11-APR-1997; 97US-0043533P.
PR 07-MAY-1997; 97WO-US007726.
PR 06-NOV-1998; 98US-00187906.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
XX
DR WPI; 2005-201184/21.
DR N-PSDB; ADY53844.
XX
PT New anti-Ret ligand (RetL) antibody, useful for treating acute renal
PT failure, acute nephritis, chronic renal failure, nephritic syndrome, as
PT well as Alzheimer's disease, Parkinson's and multiple sclerosis.
XX
PS Disclosure; SEQ ID NO 17; 66pp; English.
XX
CC The invention relates to an antibody produced by a hybridoma selected
CC from the group consisting of AA.FF9 and AA.GE7.3. The antibody is used to
CC stimulate neural and renal cell growth. This sequence corresponds to a
CC protein sequence of the invention.
XX
SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 9; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.5e-198;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240

Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300

Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
              |||||||||||||||||||||||||||||||||||||
Db        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
```

RESULT 6
ADZ00209
ID ADZ00209 standard; protein; 397 AA.
XX
AC ADZ00209;
XX
DT 30-JUN-2005 (first entry)
XX
DE Mouse Ret ligand 3 (RetL3), SEQ ID NO:17.
XX
KW Cell growth; development; signal transduction; neurological disease;
KW renal disease; genitourinary disease; neuroprotective; nephrotropic;
KW cancer; neoplasm; cytostatic; RetL3;
KW Ret tyrosine kinase receptor ligand 3; Ret ligand 3;
KW GDNF family receptor alpha 3; GFRA3.
XX
OS Mus sp.
XX
PN US2005080235-A1.
XX
PD 14-APR-2005.
XX
PF 23-SEP-2003; 2003US-00668936.
XX
PR 08-MAY-1996; 96US-0017427P.
PR 07-JUN-1996; 96US-0019300P.
PR 16-JUL-1996; 96US-0021859P.
PR 23-AUG-1996; 96US-0023444P.
PR 11-APR-1997; 97US-0043533P.
PR 07-MAY-1997; 97WO-US007726.
PR 06-NOV-1998; 98US-00187906.
XX
PA (SANI/) SANICOLA-NADEL M.
PA (HESS/) HESSION C.
PA (CATE/) CATE R L.
PA (WORL/) WORLEY D S.
XX
PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
XX
DR WPI; 2005-305025/31.
DR N-PSDB; ADZ00208.
XX
PT New polypeptide sequence that interacts with a receptor protein Ret to
PT trigger dimerization or autophosphorylation, useful in preparing a
PT composition for treating neurodegenerative disorders, e.g., Alzheimer's
PT disease.
XX
PS Claim 1; SEQ ID NO 17; 67pp; English.
XX
CC The invention relates to the murine and human RetL3 (Ret ligand 3)
CC proteins (ADZ00209 and ADZ00213, respectively) and to proteins at least
CC 80% identical to murine or human RetL3. The invention also discloses
CC other RetL proteins such as rat RetL1, human RetL1, human RetL2,
CC fragments of human RetL1, mouse RetL3 and human RetL3, and cDNA sequences
CC encoding these RetL proteins or protein fragments. Like other RetL
CC proteins, the RetL3 proteins of the invention interact with the Ret
CC receptor tyrosine kinase that is encoded by the Ret proto-oncogene,
CC triggering Ret receptor dimerization or autophosphorylation. The Ret
CC receptor is expressed during development in a variety of tissues,
CC including the peripheral and central nervous systems and the kidney. It
CC is also expressed in some cancers. RetL proteins such as the murine and
CC human RetL3 proteins, and RetL polynucleotides may be used for
CC stimulating Ret receptor signaling, thereby promoting renal or neuronal
CC cell growth or survival and minimizing damage to such tissues after
CC various insults. They may therefore be used to treat renal disorders
CC (e.g., renal failure, renal tube defects and renal trauma) or
CC neurological disorders including neurodegenerative disorders (e.g.,
CC Alzheimer's disease), bacterial or viral diseases of the nervous system
CC (e.g., meningitis), neurological damage (e.g. that caused by hemorrhage
CC or trauma) and developmental neural disorders (e.g., mental retardation).
CC Conversely, antibodies against RetL may be used to block RetL-Ret
CC receptor signal transduction for inhibiting tumor growth, fusion proteins
CC comprising a RetL protein are useful for targeting a drug to Ret receptor
CC -expressing tumors. Anti-RetL antibodies and RetL fusion proteins may
CC also be used in medical imaging. The present sequence represents a
CC specifically claimed full-length murine RetL3 protein encoded by cDNA
CC isolated in the invention.
XX
SQ Sequence 397 AA;

Query Match 100.0%; Score 2131; DB 9; Length 397;
Best Local Similarity 100.0%; Pred. No. 3.5e-198;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240

Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300

Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
              |||||||||||||||||||||||||||||||||||||
Db        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
```

RESULT 7
AAW84182
ID AAW84182 standard; protein; 397 AA.
XX
AC AAW84182;
XX
DT 25-MAR-1999 (first entry)
XX
DE A GDNFR-alpha-related protein 3 (GRR3).
XX
KW Rat; glial cell-line derived neurotrophic factor receptor; GDNFR;
KW glial cell line-derived neurotrophic factor; GDNF; neurturin;
KW signal transduction; dopaminergic nerve cell; Parkinson's disease;
KW Alzheimer's disease; amyotrophic lateral sclerosis;
KW neurological disorder; diabetes; glaucoma; sensory neuron;
KW retinal ganglion cell degeneration; sensory neuropathy; retinopathy;
KW gene therapy; GDNFR-related protein 3; GRR3.
XX
OS Rattus sp.
XX
PN WO9854213-A2.
XX
PD 03-DEC-1998.
XX
PF 27-APR-1998; 98WO-US008486.
XX
PR 30-MAY-1997; 97US-00866354.
XX
PA (AMGE-) AMGEN INC.
XX
PI Fox GM, Jing S, Wen D;
XX
DR WPI; 1999-080806/07.

```
DR   N-PSDB; AAV99331.
XX
PT   New isolated glial cell line-derived neurotrophic factor receptors - used
PT   to develop products for treating e.g. improperly functioning dopaminergic
PT   nerve cells, Parkinson's disease, Alzheimer's disease or amyotrophic
PT   lateral sclerosis.
XX
PS   Claim 51; Fig 17; 318pp; English.
XX
CC   The present sequence represents a rat glial cell-line derived
CC   neurotrophic factor receptor (GDNFR)-related protein 3 (GRR3). The
CC   protein has similar functions to GDNFR. GDNFR proteins are functionally
CC   characterised by the ability to bind glial cell line-derived neurotrophic
CC   factor (GDNF) and/or neurturin specifically, and to act as part of a
CC   molecular complex which mediates or enhances the signal transduction
CC   affects of GDNF and/or neurturin. The proteins can be used for treating
CC   improperly functioning dopaminergic nerve cells, Parkinson's disease,
CC   Alzheimer's disease or amyotrophic lateral sclerosis. They can also be
CC   used for treating neurological disorders associated with diabetes,
CC   glaucoma or other diseases and conditions involving retinal ganglion cell
CC   degeneration, sensory neuropathy caused by injury to, insults to, or
CC   degeneration of, sensory neurons, pathological conditions, or disease or
CC   injury-related retinopathies. The products can also be used for
CC   detection, diagnosis, drug screening and gene therapy
XX
SQ   Sequence 397 AA;

  Query Match             92.5%;  Score 1972;  DB 2;  Length 397;
  Best Local Similarity   92.9%;  Pred. No. 1e-182;
  Matches  369;  Conservative    9;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
              |||| ||||| |:|||||||||||||| |||| |||| ||||||||||||||||||||||
Db          1 MGLSRSPRPPPLVILLLVLSLWLPLGTGNSLPTENRLVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
              | ||| ||| |||  ||| || |||||:||||||||||||||||||||||||||||||
Db         61 LDSCTPSLSSPLPSGESATSAACLEAAQQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPV 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
              ||||||||||||||||||||||||||:||||||||||||||:||||||||||
Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLSMLKPDSDLCLKFAMLCTLNDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240

Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VAPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300

Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
              |||||||||| |||||||||||||||:||||||:||||||||||||||||||||||||||
Db        301 FISKVNTTVALGCTCRGSGNLQDECEQLEKSFSQNPCLMEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
              ||||:|||||:|||| | |||:||| || ||||||||
Db        361 TFSVMQQQNSSPALRPQLRLPVLSFFILTLILLQTLW 397


RESULT 8
AAY15182
ID   AAY15182 standard; protein; 888 AA.
XX
AC   AAY15182;
XX
DT   07-FEB-2000  (first entry)
XX
DE   gD-GFRalpha3-Rse-gD chimeric receptor.
XX
KW   gD-GFRalpha3-Rse-gD chimeric receptor; gD epitope tag; murine GFRalpha3;
KW   GPI signal; human GFRalpha3; Rse tyrosine kinase receptor; pSVi vector;
KW   recombinant PCR; SV40 promoter; agonist antibody; natural ligand.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          110. .386
FT                   /note= "Ligand binding region"
XX
PN   WO9949039-A2.
XX
PD   30-SEP-1999.
XX
PF   19-MAR-1999;   99WO-US006098.
XX
PR   23-MAR-1998;   98US-0079124P.
PR   13-APR-1998;   98US-0081569P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   De Sauvage FJ,  Klein RD,  Phillips HS,  Rosenthal A;
XX
DR   WPI; 2000-038358/03.
XX
PT   New isolated GFR-alpha3 nucleic acid, used to develop products for
PT   treating diseases or conditions involving peripheral nervous system or
PT   automic nervous system.
XX
PS   Claim 9; Page 107-110; 112pp; English.
XX
CC   The present sequence is gD-GFRalpha3-Rse-gD chimeric receptor. This was
CC   constructed with the gD epitope tag followed by the murine GFRalpha3
CC   extracellular domain (less the GPI signal; preferably the human
CC   GFRalpha3) followed by the transmembrane and intracellular domain of the
CC   Rse tyrosine kinase receptor and another gD epitope tag. This construct
CC   was assembled by recombinant PCR into a pSVi vector under the control of
CC   the SV40 promoter. This is used in an assay to identify agonist
CC   antibodies and a natural ligand for mammalian GFRalpha3
XX
SQ   Sequence 888 AA;

  Query Match             88.2%;  Score 1880;  DB 3;  Length 888;
  Best Local Similarity   94.1%;  Pred. No. 2.8e-173;
  Matches  354;  Conservative    5;  Mismatches   11;  Indels    6;  Gaps    1;

Qy         25 LGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCL 84
              | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 LEAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCL 113

Qy         85 EAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSKPWKM 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 EAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSKPWKM 173

Qy        145 NLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIRCQRHLCLAQLRSFFEKA 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 NLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIRCQRHLCLAQLRSFFEKA 233

Qy        205 AESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSRLMD 264
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        234 AESHAQGLLLCPCPPEDAGCGERRRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSRLMD 293

Qy        265 FQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDE 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 FQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDE 353

Qy        325 CEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQQNSNPALR------LQP 378
              |||||||||||||||||||||||||||||||||||||||||||||||||| |      | |
Db        354 CEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQQNSNPAWRAWVPVVLGV 413

Qy        379 RLPILSFSILPLILLQ 394
                 ::: : | ||||:
Db        414 LTALVTAAALALILLR 429


RESULT 9
```

```
AAW37465
ID   AAW37465 standard; protein; 346 AA.
XX
AC   AAW37465;
XX
DT   21-MAY-1998  (first entry)
XX
DE   Mouse Ret ligand retL3 partial sequence.
XX
KW   Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
KW   cell growth; renal cell; nerve cell; renal failure; nephritis;
KW   kidney transplant; toxic injury; hypoxic injury; neurodegeneration;
KW   motor neurone disease; multiple sclerosis; infection; meningitis;
KW   myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury;
KW   spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease;
KW   muscular dystrophy; myasthenia gravis; tumour; therapy.
XX
OS   Mus musculus.
XX
PN   WO9744356-A2.
XX
PD   27-NOV-1997.
XX
PF   07-MAY-1997;   97WO-US007726.
XX
PR   08-MAY-1996;   96US-0017427P.
PR   07-JUN-1996;   96US-0019300P.
PR   16-JUL-1996;   96US-0021859P.
PR   11-APR-1997;   97US-0043533P.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Sanicola-Nadel M,  Hession C,  Cate RL;
XX
DR   WPI; 1998-018431/02.
DR   N-PSDB; AAV00256.
XX
PT   New nucleic acid encoding ret receptor ligands and related proteins -
PT   vectors, transformed cells and antibodies, used for promoting cell growth
PT   and improving survival of injured cells, especially renal or nerve cells.
XX
PS   Disclosure; Page 73-74; 113pp; English.
XX
CC   This polypeptide comprises a partial sequence of mouse Ret ligand RetL3,
CC   deduced from EST AA050083 cDNA (see AAV00256). A full-length mouse RetL3
CC   sequence (see AAW37461) was also obtained. Rat, mouse and human retL1,
CC   retL2 and retL3 cDNA sequences (see AAV00245-51) and encoded polypeptides
CC   (see AAW37457-63) are claimed and can be used in methods for promoting
CC   cell growth and improving survival of cells, especially renal or neural
CC   cells
XX
SQ   Sequence 346 AA;

  Query Match             83.2%;  Score 1774;  DB 2;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-163;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         68 LSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 127
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 LSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 76

Qy        128 LDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 187
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 LDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 136

Qy        188 CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 247
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 196

Qy        248 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNT 307
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNT 256

Qy        308 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQ 367
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQ 316

Qy        368 QNSNPALRLQPRLPILSFSILPLILLQTLW 397
               |||||||||||||||||||||||||||||
Db        317 QNSNPALRLQPRLPILSFSILPLILLQTLW 346


RESULT 10
ADJ58707
ID   ADJ58707 standard; protein; 346 AA.
XX
AC   ADJ58707;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Murine retL3 partial protein.
XX
KW   Tissue growth; retL protein; organ failure; foetal malformation;
KW   tumour growth; renal tissue; cytostatic; vulnerary; nephrotropic; murine.
XX
OS   Mus sp.
XX
PN   US6677135-B1.
XX
PD   13-JAN-2004.
XX
PF   06-NOV-1998;   98US-00187906.
XX
PR   08-MAY-1996;   96US-0017427P.
PR   07-JUN-1996;   96US-0019300P.
PR   16-JUL-1996;   96US-0021859P.
PR   23-AUG-1996;   96US-0023444P.
PR   11-APR-1997;   97US-0043533P.
PR   07-MAY-1997;   97WO-US007726.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Sanicola-Nadel M,  Hession C,  Cate RL,  Worley DS;
XX
DR   WPI; 2004-079845/08.
DR   N-PSDB; ADJ58706.
XX
PT   New nucleic acid encoding Ret polypeptide, useful for diagnosing and/or
PT   treating diseases or conditions associated with aberrant expression or
PT   activity of the Ret ligand, such as organ failure, fetal malformations
PT   and tumor growth.
XX
PS   Disclosure; SEQ ID NO 15; 66pp; English.
XX
CC   The present invention relates to nucleotide and amino acid sequences
CC   which promote tissue growth and methods for modulating tissue growth. The
CC   invention also relates to retL proteins and polynucleotides encoding such
CC   proteins. RetL proteins interact with a receptor protein Ret to trigger
CC   dimerisation and/or autophosphorylation of the tyrosine kinase domain of
CC   the receptor protein Ret. The methods and compositions of the present
CC   invention are useful for the diagnosis and/or treatment of diseases or
CC   conditions associated with aberrant expression or activity of the Ret
CC   ligand, such as organ failure, foetal malformations and tumour growth and
CC   for promoting regeneration or survival of damaged renal tissue. The
CC   present sequence is murine retL3 partial protein of the invention.
XX
SQ   Sequence 346 AA;

  Query Match             83.2%;  Score 1774;  DB 8;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-163;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         68 LSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 127
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 LSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 76
```

```
Qy        128 LDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 LDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 136

Qy        188 CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 196

Qy        248 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNT 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNT 256

Qy        308 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQ 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQ 316

Qy        368 QNSNPALRLQPRLPILSFSILPLILLQTLW 397
              |||||||||||||||||||||||||||||
Db        317 QNSNPALRLQPRLPILSFSILPLILLQTLW 346
```

RESULT 11
ADY53843
ID ADY53843 standard; protein; 346 AA.
XX
AC ADY53843;
XX
DT 05-MAY-2005 (first entry)
XX
DE Partial mouse retL3 protein.
XX
KW DNA purification; immune stimulation; ret ligand.
XX
OS Mus sp.
XX
PN US6861509-B1.
XX
PD 01-MAR-2005.
XX
PF 21-JAN-2000; 2000US-00489407.
XX
PR 08-MAY-1996; 96US-0017427P.
PR 07-JUN-1996; 96US-0019300P.
PR 16-JUL-1996; 96US-0021859P.
PR 23-AUG-1996; 96US-0023444P.
PR 11-APR-1997; 97US-0043533P.
PR 07-MAY-1997; 97WO-US007726.
PR 06-NOV-1998; 98US-00187906.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
XX
DR WPI; 2005-201184/21.
DR N-PSDB; ADY53842.
XX
PT New anti-Ret ligand (RetL) antibody, useful for treating acute renal
PT failure, acute nephritis, chronic renal failure, nephritic syndrome, as
PT well as Alzheimer's disease, Parkinson's and multiple sclerosis.
XX
PS Disclosure; SEQ ID NO 15; 66pp; English.
XX
CC The invention relates to an antibody produced by a hybridoma selected
CC from the group consisting of AA.FF9 and AA.GE7.3. The antibody is used to
CC stimulate neural and renal cell growth. This sequence corresponds to a
CC protein sequence of the invention.
XX
SQ Sequence 346 AA;

Query Match 83.2%; Score 1774; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 1.6e-163;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         68 LSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 LSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 76

Qy        128 LDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 LDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 136

Qy        188 CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 196

Qy        248 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNT 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNT 256

Qy        308 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQ 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQ 316

Qy        368 QNSNPALRLQPRLPILSFSILPLILLQTLW 397
              |||||||||||||||||||||||||||||
Db        317 QNSNPALRLQPRLPILSFSILPLILLQTLW 346
```

RESULT 12
ADZ00207
ID ADZ00207 standard; protein; 346 AA.
XX
AC ADZ00207;
XX
DT 30-JUN-2005 (first entry)
XX
DE Mouse Ret ligand 3 (RetL3) fragment, SEQ ID NO:15.
XX
KW Cell growth; development; signal transduction; neurological disease;
KW renal disease; genitourinary disease; neuroprotective; nephrotropic;
KW cancer; neoplasm; cytostatic; RetL3;
KW Ret tyrosine kinase receptor ligand 3; Ret ligand 3;
KW GDNF family receptor alpha 3; GFRA3.
XX
OS Mus sp.
XX
PN US2005080235-A1.
XX
PD 14-APR-2005.
XX
PF 23-SEP-2003; 2003US-00668936.
XX
PR 08-MAY-1996; 96US-0017427P.
PR 07-JUN-1996; 96US-0019300P.
PR 16-JUL-1996; 96US-0021859P.
PR 23-AUG-1996; 96US-0023444P.
PR 11-APR-1997; 97US-0043533P.
PR 07-MAY-1997; 97WO-US007726.
PR 06-NOV-1998; 98US-00187906.
XX
PA (SANI/) SANICOLA-NADEL M.
PA (HESS/) HESSION C.
PA (CATE/) CATE R L.
PA (WORL/) WORLEY D S.
XX
PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
XX
DR WPI; 2005-305025/31.
DR N-PSDB; ADZ00206.
XX
PT New polypeptide sequence that interacts with a receptor protein Ret to
PT trigger dimerization or autophosphorylation, useful in preparing a
PT composition for treating neurodegenerative disorders, e.g., Alzheimer's
PT disease.
XX
PS Disclosure; SEQ ID NO 15; 67pp; English.

```
XX
CC   The invention relates to the murine and human RetL3 (Ret ligand 3)
CC   proteins (ADZ00209 and ADZ00213, respectively) and to proteins at least
CC   80% identical to murine or human RetL3. The invention also discloses
CC   other RetL proteins such as rat RetL1, human RetL1, human RetL2,
CC   fragments of human RetL1, mouse RetL3 and human RetL3, and cDNA sequences
CC   encoding these RetL proteins or protein fragments. Like other RetL
CC   proteins, the RetL3 proteins of the invention interact with the Ret
CC   receptor tyrosine kinase that is encoded by the Ret proto-oncogene,
CC   triggering Ret receptor dimerization or autophosphorylation. The Ret
CC   receptor is expressed during development in a variety of tissues,
CC   including the peripheral and central nervous systems and the kidney. It
CC   is also expressed in some cancers. RetL proteins such as the murine and
CC   human RetL3 proteins, and RetL polynucleotides may be used for
CC   stimulating Ret receptor signaling, thereby promoting renal or neuronal
CC   cell growth or survival and minimizing damage to such tissues after
CC   various insults. They may therefore be used to treat renal disorders
CC   (e.g., renal failure, renal tube defects and renal trauma) or
CC   neurological disorders including neurodegenerative disorders (e.g.,
CC   Alzheimer's disease), bacterial or viral diseases of the nervous system
CC   (e.g., meningitis), neurological damage (e.g. that caused by hemorrhage
CC   or trauma) and developmental neural disorders (e.g., mental retardation).
CC   Conversely, antibodies against RetL may be used to block RetL-Ret
CC   receptor signal transduction for inhibiting tumor growth, fusion proteins
CC   comprising a RetL protein are useful for targeting a drug to Ret receptor
CC   -expressing tumors. Anti-RetL antibodies and RetL fusion proteins may
CC   also be used in medical imaging. The present sequence represents a murine
CC   RetL3 fragment encoded by a murine RetL3 partial cDNA initially
CC   identified by a search of an expressed sequence tag (EST) database using
CC   a rat RetL1 peptide sequence, and isolated from the EST clones AA049894
CC   and AA050083.
XX
SQ   Sequence 346 AA;

  Query Match             83.2%;  Score 1774;  DB 9;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-163;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         68 LSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 127
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 LSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 76

Qy        128 LDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 LDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 136

Qy        188 CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 196

Qy        248 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNT 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNT 256

Qy        308 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQ 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQ 316

Qy        368 QNSNPALRLQPRLPILSFSILPLILLQTLW 397
              |||||||||||||||||||||||||||||
Db        317 QNSNPALRLQPRLPILSFSILPLILLQTLW 346


RESULT 13
AAW65116
ID   AAW65116 standard; protein; 400 AA.
XX
AC   AAW65116;
XX
DT   28-SEP-1998  (first entry)
XX
DE   Human GDNF alpha-3 receptor protein #1.
XX
KW   Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
KW   treatment; neurodegenerative disease; Parkinson's Disease; ALS; SMA;
KW   amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
KW   Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
KW   muscular dystrophy; diagnostic.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Protein         1. .400
FT                   /label= GDNF alpha-3
FT                   /note= "Partial sequence"
XX
PN   EP846764-A2.
XX
PD   10-JUN-1998.
XX
PF   20-NOV-1997;   97EP-00309375.
XX
PR   27-NOV-1996;   96GB-00024677.
PR   09-MAY-1997;   97GB-00009463.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Lawrence GMP;
XX
DR   WPI; 1998-299980/27.
DR   N-PSDB; AAV35364.
XX
PT   New factor alpha 3 receptor polypeptide and e.g. DNA and agonists - used
PT   to treat neuro degenerative diseases, muscular diseases and nerve and
PT   muscle trauma and in diagnostic assays.
XX
PS   Claim 4; Fig 2; 22pp; English.
XX
CC   This sequence represents a novel glial cell line-derived neurotrophic
CC   factor alpha-3 receptor (GDNF alpha-3). This protein can be used to treat
CC   e.g. neurodegenerative diseases (such as Parkinson's Disease, amyotrophic
CC   lateral sclerosis (ALS), spinal muscular atrophy (SMA), Huntington's
CC   Disease, Alzheimer's Disease, diabetic neuropathy), muscular diseases
CC   (including the muscular dystrophies) and nerve and muscle trauma and in
CC   diagnostic assays for such conditions
XX
SQ   Sequence 400 AA;

  Query Match             77.3%;  Score 1646.5;  DB 2;  Length 400;
  Best Local Similarity   77.8%;  Pred. No. 4.9e-151;
  Matches  305;  Conservative   30;  Mismatches   56;  Indels    1;  Gaps    1;

Qy          7 PRPP-LLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCT 65
              | || :||:|||:    ||| ||: | ||:| :||| |||:||:|:| | ||| || |||
Db          9 PLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRKCQADPTCSAAYHHLDSCT 68

Qy         66 SSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGD 125
              ||:| ||| || :: |||||||:|||||||| | ||||||:|  ||||||||| |||||:
Db         69 SSISTPLPSEEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGN 128

Qy        126 YELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSG 185
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        129 YELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLNDKCDRLRKAYGEACSG 188

Qy        186 IRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNC 245
              ||||:|| || :||||||| |||||||||||| | ||||||||||||:|||| | |||
Db        189 PHCQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNC 248

Qy        246 LDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKV 305
              |:||  | :||||||||:||||||||||||||||||||||||||||||||||:| |
Db        249 LELRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFVSNV 308

Qy        306 NTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVV 365
              ||:|||||||||||:||| ||  || |||| |||||||||| |||||||   ||:|:
Db        309 NTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMRFHSQLFSQDWPHPTFAVM 368
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Qy        366 QQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
              || |||:| || :| |    |||||| :||
Db        369 AHQNENPAVRPQPWVPSLFSCTLPLILLLSLW 400
```

RESULT 14
AAW37463
ID AAW37463 standard; protein; 400 AA.
XX
AC AAW37463;
XX
DT 21-MAY-1998 (first entry)
XX
DE Human Ret ligand RetL3.
XX
KW Ret ligand; RetL; RetL3; receptor; signal transduction; human;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury; neurodegeneration;
KW motor neurone disease; multiple sclerosis; infection; meningitis;
KW myelopathy; Creutzfeldt-Jakob disease; cranial nerve injury;
KW spinal cord injury; Down's syndrome; cerebral palsy; Lyme disease;
KW muscular dystrophy; myasthenia gravis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9744356-A2.
XX
PD 27-NOV-1997.
XX
PF 07-MAY-1997; 97WO-US007726.
XX
PR 08-MAY-1996; 96US-0017427P.
PR 07-JUN-1996; 96US-0019300P.
PR 16-JUL-1996; 96US-0021859P.
PR 11-APR-1997; 97US-0043533P.
XX
PA (BIOJ) BIOGEN INC.
XX
PI Sanicola-Nadel M, Hession C, Cate RL;
XX
DR WPI; 1998-018431/02.
DR N-PSDB; AAV00251.
XX
PT New nucleic acid encoding ret receptor ligands and related proteins -
PT vectors, transformed cells and antibodies, used for promoting cell growth
PT and improving survival of injured cells, especially renal or nerve cells.
XX
PS Claim 2; Page 85-86; 113pp; English.
XX
CC This amino acid sequence comprises human Ret ligand (RetL) RetL3, deduced
CC from cDNA clones (see AAV00251) isolated from a adult heart and spinal
CC cord libraries. Rat and human RetL1, human RetL2 and mouse RetL3
CC sequences (see AAW37457-62) are also claimed. Human RetL3 is 34.3%
CC identical to human RetL1, 34.9% identical to human RetL2 and 76.8%
CC identical to murine RetL3. Ret ligand is a key component of the Ret
CC signalling pathway that specifically interacts with Ret receptor protein,
CC triggering Ret dimerisation and/or autophosphorylation of the Ret
CC tyrosine kinase domain. Vectors containing retL3 DNA and prokaryotic or
CC eukaryotic host cells transformed or transfected with these vectors are
CC claimed, as well as a method for production of RetL3, its soluble
CC variants and fusion proteins with a toxin, imageable compound or
CC radionuclide. RetL3, optionally when expressed from vectors in vivo, is
CC used to promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in renal
CC failure, nephritis, kidney transplants, toxic or hypoxic injury,
CC neurodegeneration, motor neurone disease, multiple sclerosis, bacterial,
CC viral or prion infections (e.g. meningitis, myelopathy associated with
CC HIV or Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury,
CC developmental disorders such as Down's syndrome and cerebral palsy, or
CC conditions involving the peripheral nervous system (Lyme disease,
CC muscular dystrophy and myasthenia gravis). Fusion proteins are used to
CC deliver toxins etc. to Ret-expressing cells, especially tumours
XX

SQ Sequence 400 AA;

Query Match 77.3%; Score 1646.5; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 4.9e-151;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

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Qy          7 PRPP-LLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCT 65
              | || :||:|||:    ||| ||: | ||:| :||| |||:||:|:| | ||| || |||
Db          9 PLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRKCQADPTCSAAYHHLDSCT 68

Qy         66 SSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGD 125
              ||:| ||| || :: |||||||:|||||||| | ||||||:|  ||||||||| |||||:
Db         69 SSISTPLPSEEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGN 128

Qy        126 YELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSG 185
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        129 YELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLNDKCDRLRKAYGEACSG 188

Qy        186 IRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNC 245
              ||||:|| || :||||||| |||||||||||| | ||||||||||||:|||| | |||
Db        189 PHCQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNC 248

Qy        246 LDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKV 305
              |:||  | :|||||||:|||||||||||||||||||||||||||||||||||||:| |
Db        249 LELRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFVSNV 308

Qy        306 NTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVV 365
              ||:|||||||||||:||| ||  || |||| |||||||||| |||||||   ||:|:
Db        309 NTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMRFHSQLFSQDWPHPTFAVM 368

Qy        366 QQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
              || |||:| || :| |    |||||| :||
Db        369 AHQNENPAVRPQPWVPSLFSCTLPLILLLSLW 400
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RESULT 15
AAW84186
ID AAW84186 standard; protein; 400 AA.
XX
AC AAW84186;
XX
DT 25-MAR-1999 (first entry)
XX
DE Glial cell line-derived neurotrophic factor receptor gamma 2.
XX
KW Glial cell line-derived neurotrophic factor receptor gamma 2;
KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gamma2;
KW Parkinson's disease; schizophrenia; insomnia; tardive dyskenisia;
KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
KW renal disorder; kidney failure; gut dysfunction; regeneration;
KW cardiomyocyte; epithelium; hepatocyte.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .31
FT /label= signal_peptide
FT Protein 32. .400
FT /label= mature_protein
FT Domain 32. .382
FT /note= "extracellular domain"
FT Domain 383. .400
FT /note= "transmembrane domain"
XX
PN WO9853069-A2.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98WO-US010328.
XX
PR 20-MAY-1997; 97US-0047092P.
PR 27-JUN-1997; 97US-00884638.

XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Hsu T, Young P, Gentz RL, Ruben SM;
XX
DR WPI; 1999-070150/06.
DR N-PSDB; AAV99334.
XX
PT New isolated glial cell derived neurotrophic factor receptors - used to
PT develop products for treating e.g. neurodegenerative disorders,
PT schizophrenia, hypertension, tumours, renal disorders, kidney failure or
PT gut dysfunction.
XX
PS Claim 53; Fig 7A-D; 156pp; English.
XX
CC The present sequence represents a glial cell line-derived neurotrophic
CC factor receptor gamma 2 (GDNFR-gamma2). GDNFR-gamma2 shares high homology
CC with GDNFR-alpha, which is capable of complexing with glial cell line-
CC derived neurotrophic factor (GDNF) and mediating cell response to GDNF.
CC The GDNFR polypeptides and agonists can be used for treating disorders
CC associated with decreased activity of the respective polypeptides. They
CC can be used for treating neurodegenerative diseases such as amyotrophic
CC lateral sclerosis, Parkinson's disease, schizophrenia, insomnia, tardive
CC dyskenisia, hypertension, pituitary adenomas, hyperprolactinemia, thyroid
CC tumour, renal disorders, kidney failure, gut dysfunction, or for
CC regeneration of cardiomyocytes, epithelium or hepatocytes. Antagonists of
CC the polypeptides can be used for treating disorders associated with
CC increased activity of the respective polypeptides. The products can also
CC be used for detection, diagnosis and drug screening.
XX
SQ Sequence 400 AA;

Query Match 77.3%; Score 1646.5; DB 2; Length 400;
Best Local Similarity 77.8%; Pred. No. 4.9e-151;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

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Qy          7 PRPP-LLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCT 65
              | || :||:|||:    ||| ||: | ||:| :||| |||:||:|:| | ||| || |||
Db          9 PLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRKCQADPTCSAAYHHLDSCT 68

Qy         66 SSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGD 125
              ||:| ||| || :: |||||||:|||||||| | |||||||:|  ||||||||| |||||:
Db         69 SSISTPLPSEEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGN 128

Qy        126 YELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSG 185
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        129 YELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLNDKCDRLRKAYGEACSG 188

Qy        186 IRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNC 245
              ||||:|| || :||||||| |||||||||||| | ||||||||||||:|||| | |||
Db        189 PHCQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNC 248

Qy        246 LDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKV 305
              |:||  | :|||||||||:|||||||||||||||||||||||||||||||||||:| |
Db        249 LELRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFVSNV 308

Qy        306 NTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVV 365
              ||:|||||||||||:||| ||  || |||| |||||||||| |||||||   ||:|:
Db        309 NTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMRFHSQLFSQDWPHPTFAVM 368

Qy        366 QQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
              || |||:| || :| |    |||||| :||
Db        369 AHQNENPAVRPQPWVPSLFSCTLPLILLLSLW 400
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Search completed: March 7, 2006, 23:31:54
Job time : 70.6336 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 7, 2006, 23:31:14 ; Search time 55.126 Seconds
(without alignments)
3009.073 Million cell updates/sec

Title: US-10-621-855-5
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLLMILLLVLS.....PRLPILSFSILPLILLQTLW 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2131	100.0	397	3	US-09-220-920-64	Sequence 64, Appl
2	2131	100.0	397	5	US-10-668-936-17	Sequence 17, Appl
3	2131	100.0	397	5	US-10-621-855-5	Sequence 5, Appli
4	1972	92.5	397	5	US-10-872-161-42	Sequence 42, Appl
5	1880	88.2	888	5	US-10-621-855-20	Sequence 20, Appl
6	1774	83.2	346	5	US-10-668-936-15	Sequence 15, Appl
7	1646.5	77.3	400	3	US-09-220-920-63	Sequence 63, Appl
8	1646.5	77.3	400	3	US-09-828-366-16	Sequence 16, Appl
9	1646.5	77.3	400	5	US-10-668-936-21	Sequence 21, Appl
10	1646.5	77.3	400	5	US-10-621-855-15	Sequence 15, Appl
11	1646.5	77.3	628	5	US-10-621-855-18	Sequence 18, Appl
12	1643.5	77.1	400	5	US-10-482-029-275	Sequence 275, App
13	1642.5	77.1	400	5	US-10-872-161-38	Sequence 38, Appl
14	1458	68.4	369	5	US-10-621-855-17	Sequence 17, Appl
15	1386	65.0	315	5	US-10-668-936-19	Sequence 19, Appl
16	654	30.7	498	5	US-10-872-161-43	Sequence 43, Appl
17	640.5	30.1	489	5	US-10-872-161-44	Sequence 44, Appl
18	577.5	27.1	445	4	US-10-673-007-11	Sequence 11, Appl
19	577.5	27.1	460	5	US-10-872-161-40	Sequence 40, Appl
20	577.5	27.1	464	3	US-09-388-316-6	Sequence 6, Appli
21	577.5	27.1	464	4	US-10-357-822-6	Sequence 6, Appli
22	577.5	27.1	464	4	US-10-673-007-2	Sequence 2, Appli
23	577.5	27.1	464	5	US-10-621-855-9	Sequence 9, Appli
24	577.5	27.1	664	3	US-09-388-316-18	Sequence 18, Appl
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26	577.5	27.1	951	5	US-10-621-855-19	Sequence 19, Appl
27	574.5	27.0	464	3	US-09-388-316-3	Sequence 3, Appli
28	574.5	27.0	464	4	US-10-357-822-3	Sequence 3, Appli
29	574.5	27.0	464	4	US-10-673-007-9	Sequence 9, Appli
30	574.5	27.0	464	5	US-10-872-161-36	Sequence 36, Appl
31	574.5	27.0	464	5	US-10-723-860-3950	Sequence 3950, Ap
32	574.5	27.0	464	5	US-10-668-936-13	Sequence 13, Appl
33	574.5	27.0	464	5	US-10-621-855-7	Sequence 7, Appli
34	574.5	27.0	664	3	US-09-388-316-16	Sequence 16, Appl
35	574.5	27.0	664	4	US-10-357-822-16	Sequence 16, Appl
36	515	24.2	460	4	US-10-241-220-62	Sequence 62, Appl
37	515	24.2	460	5	US-10-872-972-62	Sequence 62, Appl
38	515	24.2	460	5	US-10-872-991-62	Sequence 62, Appl
39	515	24.2	460	5	US-10-668-936-11	Sequence 11, Appl
40	515	24.2	460	5	US-10-621-855-6	Sequence 6, Appli
41	513.5	24.1	463	4	US-10-155-693-10	Sequence 10, Appl
42	513.5	24.1	463	4	US-10-155-693-12	Sequence 12, Appl
43	513.5	24.1	463	5	US-10-872-161-10	Sequence 10, Appl
44	513.5	24.1	463	5	US-10-872-161-12	Sequence 12, Appl
45	513.5	24.1	465	4	US-10-357-822-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-220-920-64
; Sequence 64, Application US/09220920
; Patent No. US20020002269A1
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. US20020002269A1el Neurotrophic Factor
; FILE REFERENCE: 6029-7996
; CURRENT APPLICATION NUMBER: US/09/220,920
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Murine
US-09-220-920-64

Query Match 100.0%; Score 2131; DB 3; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.6e-182;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
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Db          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
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Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
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Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
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Db        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240

Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300

Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
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Db        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
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Db        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
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RESULT 2
US-10-668-936-17
; Sequence 17, Application US/10668936
; Publication No. US20050080235A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/668,936
; FILING DATE: 23-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/187,906
; FILING DATE: 06-NOV-1998
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-668-936-17

Query Match 100.0%; Score 2131; DB 5; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.6e-182;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
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Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
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Db        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300

Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
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Db        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
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Db        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
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RESULT 3
US-10-621-855-5
; Sequence 5, Application US/10621855
; Publication No. US20050221330A1
; GENERAL INFORMATION:
; APPLICANT: De Sauvage, Frederic J.
; APPLICANT: Klein, Richard D.
; APPLICANT: Rosenthal, Arnon
; APPLICANT: Phillips, Heidi S.
; TITLE OF INVENTION: GFRALPHA3 AND ITS USES
; FILE REFERENCE: GENENT.065A
; CURRENT APPLICATION NUMBER: US/10/621,855
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 09/272,835
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/079,124
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 60/081,569
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-621-855-5

Query Match 100.0%; Score 2131; DB 5; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.6e-182;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
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Db          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
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Db         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240

Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
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Db        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
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Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
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Db        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
              |||||||||||||||||||||||||||||||||||||
Db        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397


RESULT 4
US-10-872-161-42
; Sequence 42, Application US/10872161
; Publication No. US20040235714A1
; GENERAL INFORMATION:
;  APPLICANT: FOX, GARY M.
;  APPLICANT:  JING, SHUQIAN
;  APPLICANT:  WEN, DUANZHI
;  TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
;  FILE REFERENCE: A-401D
;  CURRENT APPLICATION NUMBER: US/10/872,161
;  CURRENT FILING DATE:  2004-06-18
;  PRIOR APPLICATION NUMBER: US/08/866,354
;  PRIOR FILING DATE: 1997-05-30
;  PRIOR APPLICATION NUMBER: US 60/015,907
;  PRIOR FILING DATE: 1996-04-22
;  PRIOR APPLICATION NUMBER: US 60/017,221
;  PRIOR FILING DATE: 1996-05-09
;  PRIOR APPLICATION NUMBER: US 08/837,199
;  PRIOR FILING DATE: 1997-04-14
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
;   LENGTH: 397
;   TYPE: PRT
;   ORGANISM: RAT
US-10-872-161-42

  Query Match             92.5%;  Score 1972;  DB 5;  Length 397;
  Best Local Similarity   92.9%;  Pred. No. 4.6e-168;
  Matches  369;  Conservative    9;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
              |||| ||||| |:||||||||||||| |||| |||| ||||||||||||||||||||||
Db          1 MGLSRSPRPPPLVILLLVLSLWLPLGTGNSLPTENRLVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
              | ||| ||| |||  ||| || |||||:||||||||||||||||||||||||||||||
Db         61 LDSCTPSLSSPLPSGESATSAACLEAAQQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPV 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
              ||||||||||||||||||||||||||:||||||||||||||:||||||||||||
Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLSMLKPDSDLCLKFAMLCTLNDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240

Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VAPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300

Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
              |||||||||||| ||||||||||||||||||:||||||||:||||||||||||||||||||
Db        301 FISKVNTTVALGCTCRGSGNLQDECEQLEKSFSQNPCLMEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
              ||||:|||||:|||| | |||:||| || ||||||||
Db        361 TFSVMQQQNSSPALRPQLRLPVLSFFILTLILLQTLW 397


RESULT 5
US-10-621-855-20
; Sequence 20, Application US/10621855
; Publication No. US20050221330A1
; GENERAL INFORMATION:
;  APPLICANT: De Sauvage, Frederic J.
;  APPLICANT:  Klein, Richard D.
;  APPLICANT:  Rosenthal, Arnon
;  APPLICANT:  Phillips, Heidi S.
;  TITLE OF INVENTION: GFRALPHA3 AND ITS USES
;  FILE REFERENCE: GENENT.065A
;  CURRENT APPLICATION NUMBER: US/10/621,855
;  CURRENT FILING DATE:  2003-07-16
;  PRIOR APPLICATION NUMBER: 09/272,835
;  PRIOR FILING DATE: 1999-03-19
;  PRIOR APPLICATION NUMBER: 60/079,124
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: 60/081,569
;  PRIOR FILING DATE: 1998-04-13
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 888
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chimeric receptor comprising murine sequence.
US-10-621-855-20

  Query Match             88.2%;  Score 1880;  DB 5;  Length 888;
  Best Local Similarity   94.1%;  Pred. No. 2.2e-159;
  Matches  354;  Conservative    5;  Mismatches   11;  Indels    6;  Gaps    1;

Qy         25 LGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCL 84
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 LEAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCL 113

Qy         85 EAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSKPWKM 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 EAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSKPWKM 173

Qy        145 NLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIRCQRHLCLAQLRSFFEKA 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 NLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIRCQRHLCLAQLRSFFEKA 233

Qy        205 AESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSRLMD 264
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        234 AESHAQGLLLCPCPPEDAGCGERRRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSRLMD 293

Qy        265 FQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDE 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 FQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDE 353

Qy        325 CEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQQNSNPALR------LQP 378
              |||||||||||||||||||||||||||||||||||||||||||||||| |      |
Db        354 CEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQQNSNPAWRAWVPVVLGV 413

Qy        379 RLPILSFSILPLILLQ 394
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Db        414 LTALVTAAALALILLR 429


RESULT 6
US-10-668-936-15
; Sequence 15, Application US/10668936
; Publication No. US20050080235A1
;   GENERAL INFORMATION:
;        APPLICANT: BIOGEN, INC.
;        TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
;                            and Renal Growth
;        NUMBER OF SEQUENCES: 21
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Biogen, Inc.
;             STREET: 14 Cambridge Center
;             CITY: Cambridge
;             STATE: MA
```

```
;             COUNTRY: USA
;             ZIP: 02142
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/668,936
;             FILING DATE: 23-Sep-2003
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 09/187,906
;             FILING DATE: 06-NOV-1998
;             APPLICATION NUMBER: PCT/US97/07726
;             FILING DATE: 07-MAY-97
;             APPLICATION NUMBER: US 60/017,427
;             FILING DATE: 08-MAY-96
;             APPLICATION NUMBER: US 60/019,300
;             FILING DATE: 07-JUN-96
;             APPLICATION NUMBER: US 60/021,859
;             FILING DATE: 16-JUL-96
;             APPLICATION NUMBER: US 60/043,533
;             FILING DATE: 10-APR-97
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Kaplan, Warren A.
;             REGISTRATION NUMBER: 34,199
;             REFERENCE/DOCKET NUMBER: A008 PCT CIP
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617-679-2400
;             TELEFAX: 617-679-2838
;   INFORMATION FOR SEQ ID NO: 15:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 346 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-668-936-15

  Query Match             83.2%;  Score 1774;  DB 5;  Length 346;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-150;
  Matches  330;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         68 LSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 127
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Db         17 LSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYE 76

Qy        128 LDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 LDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIR 136

Qy        188 CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 CQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLD 196

Qy        248 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNT 307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 LRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNT 256

Qy        308 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQ 367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 TVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQ 316

Qy        368 QNSNPALRLQPRLPILSFSILPLILLQTLW 397
              |||||||||||||||||||||||||||||
Db        317 QNSNPALRLQPRLPILSFSILPLILLQTLW 346


RESULT 7
US-09-220-920-63
; Sequence 63, Application US/09220920
; Patent No. US20020002269A1
; GENERAL INFORMATION:
;  APPLICANT: Milbrandt, Jeffrey D.
;  APPLICANT: Baloh, Robert H.
;  TITLE OF INVENTION: Artemin, A No. US20020002269A1el Neurotrophic Factor
;  FILE REFERENCE: 6029-7996
;  CURRENT APPLICATION NUMBER: US/09/220,920
;  CURRENT FILING DATE: 1998-12-24
;  EARLIER APPLICATION NUMBER: 09/163,283
;  EARLIER FILING DATE: 1998-09-29
;  EARLIER APPLICATION NUMBER: 60/108,148
;  EARLIER FILING DATE: 1998-11-12
;  EARLIER APPLICATION NUMBER: 09/218,698
;  EARLIER FILING DATE: 1998-12-22
;  NUMBER OF SEQ ID NOS: 120
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
;   LENGTH: 400
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-220-920-63

  Query Match             77.3%;  Score 1646.5;  DB 3;  Length 400;
  Best Local Similarity   77.8%;  Pred. No. 7.2e-139;
  Matches  305;  Conservative   30;  Mismatches   56;  Indels    1;  Gaps    1;

Qy          7 PRPP-LLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCT 65
              | || :||:|||:    ||| ||: | ||:| :||| |||:||:|:| | ||| || |||
Db          9 PLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRKCQADPTCSAAYHHLDSCT 68

Qy         66 SSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGD 125
              ||:| ||| || :: |||||||:|||||||| | |||||||:|  |||||||||| |||||:
Db         69 SSISTPLPSEEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGN 128

Qy        126 YELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSG 185
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        129 YELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLNDKCDRLRKAYGEACSG 188

Qy        186 IRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNC 245
              ||||:|| || :||||||| |||||||||||| | ||||||||||||:|||| | |||
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Qy        246 LDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKV 305
              |:||  | :||||||||:|||||||||||||||||||||||||||||||||||||:| |
Db        249 LELRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFVSNV 308

Qy        306 NTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVV 365
              ||:|||||||||||:||| ||  || |||| ||||||||| |||||||   ||:|:
Db        309 NTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMRFHSQLFSQDWPHPTFAVM 368

Qy        366 QQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
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Db        369 AHQNENPAVRPQPWVPSLFSCTLPLILLLSLW 400


RESULT 8
US-09-828-366-16
; Sequence 16, Application US/09828366
; Patent No. US20020010137A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Klein, Robert D.
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Yuan,Jean
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
;  TITLE OF INVENTION:  CELL GROWTH
;  FILE REFERENCE: P1694R1C1
;  CURRENT APPLICATION NUMBER: US/09/828,366
;  CURRENT FILING DATE:  2001-04-05
;  Prior filing data removed - refer to PALM or file wrapper
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 7, 2006, 23:31:54 ; Search time 6.94866 Seconds
(without alignments)
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Title: US-10-621-855-5
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLLMILLLVLS.....PRLPILSFSILPLILLQTLW 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	132	6.2	4544	7	US-11-076-427A-32	Sequence 32, Appl
2	123	5.8	1170	7	US-11-114-962-5	Sequence 5, Appli
3	118.5	5.6	2556	7	US-11-050-346-67	Sequence 67, Appl
4	114.5	5.4	1433	7	US-11-114-962-1	Sequence 1, Appli
5	108.5	5.1	1268	6	US-10-453-372-1144	Sequence 1144, Ap
6	108.5	5.1	1268	6	US-10-453-372-1154	Sequence 1154, Ap
7	108.5	5.1	1288	6	US-10-453-372-1146	Sequence 1146, Ap
8	108.5	5.1	1288	6	US-10-453-372-1152	Sequence 1152, Ap
9	108	5.1	1400	6	US-10-821-234-1045	Sequence 1045, Ap
10	106	5.0	2911	7	US-11-090-617-706	Sequence 706, App
11	105.5	5.0	401	7	US-11-072-175-224	Sequence 224, App
12	104	4.9	1193	7	US-11-022-478-8	Sequence 8, Appli
13	103	4.8	1379	7	US-11-114-962-4	Sequence 4, Appli
14	102	4.8	999	7	US-11-113-424-36	Sequence 36, Appl
15	102	4.8	1218	7	US-11-078-735-20	Sequence 20, Appl
16	102	4.8	1218	7	US-11-050-346-65	Sequence 65, Appl
17	102	4.8	1218	7	US-11-103-077-20	Sequence 20, Appl
18	102	4.8	1218	7	US-11-072-175-155	Sequence 155, App
19	102	4.8	1218	7	US-11-022-478-4	Sequence 4, Appli
20	101	4.7	997	7	US-11-080-991-50	Sequence 50, Appl
21	100	4.7	728	7	US-11-022-478-11	Sequence 11, Appl
22	100	4.7	969	6	US-10-055-877-214	Sequence 214, App
23	100	4.7	1620	6	US-10-453-372-868	Sequence 868, App
24	99.5	4.7	712	7	US-11-050-857-952	Sequence 952, App
25	99.5	4.7	806	7	US-11-050-857-951	Sequence 951, App
26	99.5	4.7	970	7	US-11-050-857-950	Sequence 950, App
27	99.5	4.7	1083	7	US-11-050-857-949	Sequence 949, App
28	99.5	4.7	1292	7	US-11-050-857-948	Sequence 948, App
29	99.5	4.7	1346	7	US-11-050-857-947	Sequence 947, App
30	99.5	4.7	1419	7	US-11-114-962-3	Sequence 3, Appli
31	99.5	4.7	1564	7	US-11-050-857-943	Sequence 943, App
32	99.5	4.7	1655	7	US-11-050-857-942	Sequence 942, App
33	99.5	4.7	1658	7	US-11-050-857-935	Sequence 935, App
34	99.5	4.7	1673	7	US-11-050-857-936	Sequence 936, App
35	99.5	4.7	1730	7	US-11-050-857-946	Sequence 946, App
36	99.5	4.7	1837	7	US-11-050-857-940	Sequence 940, App
37	99.5	4.7	1928	7	US-11-050-857-939	Sequence 939, App
38	99.5	4.7	2065	7	US-11-050-857-945	Sequence 945, App
39	99.5	4.7	2067	7	US-11-050-857-944	Sequence 944, App
40	99.5	4.7	2091	7	US-11-050-857-941	Sequence 941, App
41	99.5	4.7	2110	7	US-11-050-857-937	Sequence 937, App
42	99.5	4.7	2110	7	US-11-050-857-938	Sequence 938, App
43	99.5	4.7	2201	7	US-11-050-857-1150	Sequence 1150, Ap
44	99.5	4.7	2293	7	US-11-050-857-934	Sequence 934, App
45	97.5	4.6	3635	7	US-11-019-711-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-11-076-427A-32
; Sequence 32, Application US/11076427A
; Publication No. US20060025338A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, et al.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENOU
; TITLE OF INVENTION: VESSEL ARTERIALIZATION
; FILE REFERENCE: 28967/40008A
; CURRENT APPLICATION NUMBER: US/11/076,427A
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,581
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 4544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-427A-32

Query Match 6.2%; Score 132; DB 7; Length 4544;
Best Local Similarity 20.2%; Pred. No. 0.0011;
Matches 78; Conservative 35; Mismatches 142; Indels 132; Gaps 20;

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Qy        62 GSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRM----------KHQATCL 111
             |:|  : ||          || :|:::: | |  ||  : |:           :  : |
Db      2615 GTCIGNSSR------CNQFVDCEDASDEM-NCSATDCSSYFRLGVKGVLFQPCERTSLCY 2667

Qy       112 DIYWTVHPARSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDK 171
             .  |    |  ||       | |        |     ||     |  |: :  |   |
Db      2668 APSWVCDGANDCGD-------YSDERDCPGVKRPRCPLNYFACPSGRCIPMSWTCDKEDD 2720

Qy       172 CDRLRKAYGE-------ACS--GIRCQRHLCLAQ---------LRSFFEKAAESHAQG-- 211
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Db      2721 CE-----HGEDETHCNKFCSEAQFECQNHRCISKQWLCDGSDDCGDGSDEAA--HCEGKT 2773

Qy       212 ----LLLCP----CAPE------DAGCGERRRNTIAPSCALPSVTPN---------CLDL 248
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Qy       249 RSFCRAD---------------PLC---------------RSRLMDFQTHCHPMDILGT- 277
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Db      2834 HFVCDHDRDCADGSDESPECEYPTCGPSEFRCANGRCLSSRQWECDGENDCHDQSDEAPK 2893

Qy       278 ---CATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDEC--EQLERSF 332
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Db      2894 NPHCTSPEHKC----------NASSQFLCSSGRCVAEALLCNG----QDDCGDSSDERGC 2939
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Qy        333 SQNPCLVEAIAAKMRFHRQLFSQDWAD 359
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Db       2940 HINECLSRKLSG--------CSQDCED 2958


RESULT 2
US-11-114-962-5
; Sequence 5, Application US/11114962
; Publication No. US20060030694A1
; GENERAL INFORMATION:
;  APPLICANT: Kitajewski, Jan
;  APPLICANT:  Shawber, Carrie
;  APPLICANT:  Funahashi, Yasuhiro
;  TITLE OF INVENTION: Notch-Based Fusion Proteins And Uses Thereof
;  FILE REFERENCE: 0575/71308-A
;  CURRENT APPLICATION NUMBER: US/11/114,962
;  CURRENT FILING DATE:  2005-04-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
;   LENGTH: 1170
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-114-962-5

  Query Match             5.8%;  Score 123;  DB 7;  Length 1170;
  Best Local Similarity   22.6%;  Pred. No. 0.0015;
  Matches   81;  Conservative   33;  Mismatches  156;  Indels   88;  Gaps   19;

Qy         40 SCTQARKKCEANP--------------ACKAAYQHLG-SCTSSLSRPLPLEESAMSADCL 84
              :|::    | : |              :|    | |  | :::      :  :|| ||
Db        722 TCSEEVTACHSGPCLNGGSCSIRPEGYSCTCLPSHTGRHCQTAV-------DHCVSASCL 774

Qy         85 EA----------------------AEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARS 122
                                      |:  | |  |  |    :::||| |   |   ||
Db        775 NGGTCVNKPGTFFCLCATGFQGLHCEEKTNPSCADSPC----RNKATCQD---TPRGARC 827

Qy        123 L---GDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLK--FAMLCTLHDKCDRLRK 177
              |   |          |    ||       |        |||:     ||      | :
Db        828 LCSPGYTGSSCQTLIDLCARKPCPHTARCLQSGPSFQCLCLQGWTGALCDFPLSCQKAAM 887

Qy        178 AYGEACSGIRCQR-HLCLAQLRSFFEKAAESHAQGLL----LCPCAPEDAGCGERRRNTI 232
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Db        888 SQGIEISGL-CQNGGLCIDTGSSYFCRCPPGF-QGKLCQDNVNPCEPNPCHHG----STC 941

Qy        233 AP-------SCALPSVTPNCLDLRSFCRADP-----LCRSRLMDFQTHCHPMDILGTCAT 280
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Db        942 VPQPSGYVCQCAPGYEGQNCSKVLDACQSQPCHNHGTCTSRPGGFHCACPPGFVGLRCEG 1001

Qy        281 EQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDECEQLERSFSQN-PC 337
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Db       1002 DVDECLDRPCHPSGTAACHSLAN------AFYCQCL-PGHTGQRCE-VEMDLCQSQPC 1051


RESULT 3
US-11-050-346-67
; Sequence 67, Application US/11050346
; Publication No. US20060002924A1
; GENERAL INFORMATION:
;  APPLICANT: BODMER, MARK WILLIAM
;  APPLICANT:  CHAMPION, BRIAN ROBERT
;  APPLICANT:  LENNARD, ANDREW CHRISTOPHER
;  APPLICANT:  MCKENZIE, GRAHAME JAMES
;  APPLICANT:  TUGAL, TAMARA
;  APPLICANT:  WARD, GEORGE ALBERT
;  TITLE OF INVENTION: CONJUGATE OF NOTCH SIGNALLING PATHWAY MODULATORS AND
;  TITLE OF INVENTION:  THEIR USE IN MEDICAL TREATMENT
;  FILE REFERENCE: 674525-2016
;  CURRENT APPLICATION NUMBER: US/11/050,346
;  CURRENT FILING DATE:  2005-02-03
;  PRIOR APPLICATION NUMBER: GB 0312062.3
;  PRIOR FILING DATE: 2003-05-24
;  PRIOR APPLICATION NUMBER: PCT/GB03/01525
;  PRIOR FILING DATE: 2003-04-04
;  PRIOR APPLICATION NUMBER: GB 0300234.2
;  PRIOR FILING DATE: 2003-01-07
;  PRIOR APPLICATION NUMBER: GB 0218068.5
;  PRIOR FILING DATE: 2002-08-03
;  PRIOR APPLICATION NUMBER: GB 0220849.4
;  PRIOR FILING DATE: 2002-09-07
;  PRIOR APPLICATION NUMBER: GB 0220912.0
;  PRIOR FILING DATE: 2002-09-10
;  PRIOR APPLICATION NUMBER: GB 0220913.8
;  PRIOR FILING DATE: 2002-09-10
;  PRIOR APPLICATION NUMBER: PCT/GB02/05137
;  PRIOR FILING DATE: 2002-11-13
;  PRIOR APPLICATION NUMBER: PCT/GB02/05133
;  PRIOR FILING DATE: 2002-11-13
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 67
;   LENGTH: 2556
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (89)
;   OTHER INFORMATION: Variable amino acid
US-11-050-346-67

  Query Match             5.6%;  Score 118.5;  DB 7;  Length 2556;
  Best Local Similarity   20.1%;  Pred. No. 0.01;
  Matches   84;  Conservative   48;  Mismatches  135;  Indels  151;  Gaps   26;

Qy         39 NSCTQARKKCEANPACKAAYQHLGSCTSSLSRPL---PLEESAMSAD-CLEAAEQLRNSS 94
              | | :    |: ||     |   : :| |  : |      ::| :: |: |  | : :
Db        379 NPCNEG-SNCDTNPVNGKA---ICTCPSGYTGPACSQDVDECSLGANPCEHAGKCINTLG 434

Qy         95 LIDCRC-----------------HRRMKHQATCLDIYWTVHPARSLGDYELDVSP-YE-- 134
              :|:|                 ::  |||||          :|:::    | ||
Db        435 SFECQCLQGYTGPRCEIDVNECVSNPCQNDATCLD---------QIGEFQCMCMPGYEGV 485

Qy        135 ------DTVTSKPWKMN---LSKLN-------------MLKPDSDLCLK----------- 161
                   |   | |   |    | |:|                : : | | |
Db        486 HCEVNTDECASSPCLHNGRCLDKINEFQCECPTGFTGHLCQYDVDECASTPCKNGAKCLD 545

Qy        162 ----FAMLCT-----LH-----DKCDRLRKAYGEACSGIRCQRHLCLAQLRSFFEKAAES 207
                  : :||       |      |:||      ||     |:     ||      :     |:
Db        546 GPNTYTCVCTEGYTGTHCEVDIDECDPDPCHYGSCKDGVATFTCLCRP---GYTGHHCET 602

Qy        208 HAQGLLLCPCA-------PEDAGCGERRRNTIAPSCAL--------PSVTPNCLD-LRSF 251
              :            ||      |::|      : |  |:| :         |  :  ||| :  :
Db        603 NINECSSQPCRLRGTCQDPDNAYLCFCLKGTTGPNCEINLDDCASSPCDSGTCLDKIDGY 662

Qy        252 -CRADP-----LCRSRLMDFQTH-CHPMDILGTCATE----QSRCLRAYLGLIGTAMTPN 300
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Db        663 ECACEPGYTGSMCNSNIDECAGNPCHNG---GTCEDGINGFTCRCPEGY-------HDPT 712

Qy        301 FISKVNTTVALSC---TCRGSGN----------------LQDECEQLERSFSQNPCL 338
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Db        713 CLSEVNECNSNPCVHGACRDSLNGYKCDCDPGWSGTNCDINNNECE-------SNPCV 763


RESULT 4
US-11-114-962-1
; Sequence 1, Application US/11114962
; Publication No. US20060030694A1
; GENERAL INFORMATION:
;  APPLICANT: Kitajewski, Jan
;  APPLICANT:  Shawber, Carrie
;  APPLICANT:  Funahashi, Yasuhiro
;  TITLE OF INVENTION: Notch-Based Fusion Proteins And Uses Thereof
;  FILE REFERENCE: 0575/71308-A
;  CURRENT APPLICATION NUMBER: US/11/114,962
;  CURRENT FILING DATE:  2005-04-26
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 7, 2006, 23:30:09 ; Search time 14.3606 Seconds
(without alignments)
2659.928 Million cell updates/sec

Title: US-10-621-855-5
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLLMILLLVLS.....PRLPILSFSILPLILLQTLW 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2131	100.0	397	2	JE0082	GPI-linked recepto
2	132	6.2	4544	1	S02392	alpha-2-macroglobu
3	131	6.1	4545	1	S25111	alpha-2-macroglobu
4	124	5.8	1722	2	E89753	protein F11C7.4 [i
5	123	5.8	1964	2	T09059	notch4 - mouse
6	120.5	5.7	2531	2	A46019	notch-1 protein -
7	118	5.5	2555	2	A40043	notch protein homo
8	117	5.5	1746	1	S19694	tenascin precursor
9	117	5.5	4543	1	A53102	alpha-2-macroglobu
10	114.5	5.4	2531	2	S18188	notch protein homo
11	114	5.3	2437	2	S42612	transmembrane prot
12	112.5	5.3	2703	1	A24420	notch protein - fr
13	110	5.2	965	2	S62935	hypothetical prote
14	110	5.2	1187	2	T18355	hypothetical prote
15	110	5.2	2321	2	S78549	notch3 protein - h
16	109.5	5.1	2233	2	T28669	surface protein 51
17	109	5.1	1047	2	D71302	probable exonuclea
18	108	5.1	1394	2	A35626	transforming growt
19	108	5.1	1712	2	A38261	masking protein pr
20	108	5.1	1847	2	T18308	probable vitelloge
21	107.5	5.0	996	2	JE0237	apolipoprotein E r
22	107.5	5.0	2150	2	T32497	hypothetical prote
23	107	5.0	3051	2	S42373	hypothetical prote
24	106.5	5.0	2019	1	JQ1322	tenascin precursor
25	106	5.0	2918	2	A54105	fibrillin-2 precur
26	105.5	5.0	384	2	S25771	gas1 protein - mou
27	105.5	5.0	873	1	A49729	VLDL receptor prec
28	105	4.9	1077	2	T41146	probable cysteine-
29	105	4.9	1106	2	T13938	gene shuttle craft
30	105	4.9	1408	2	S16148	gene serrate prote
31	104.5	4.9	1203	2	A49175	Motch B protein -
32	103.5	4.9	869	1	JC4858	VLDL receptor prec
33	103	4.8	886	2	A57172	probable hormone r
34	103	4.8	2318	2	S45306	notch 3 protein -
35	102.5	4.8	835	2	JP0076	nel protein - chic
36	102.5	4.8	1188	2	D86236	protein F14N23.5 [
37	102	4.8	1220	2	A56136	jagged protein pre
38	101.5	4.8	593	1	GYHU	granulin precursor
39	100.5	4.7	5376	2	T42215	zonadhesin - mouse
40	100	4.7	728	2	I50719	C-Delta-1 - chicke
41	100	4.7	1106	2	T44598	hypothetical prote
42	99.5	4.7	2471	2	A49128	cell-fate determin
43	99.5	4.7	2718	2	A23475	G surface protein
44	99	4.6	2704	2	S09118	G surface protein
45	99	4.6	2907	2	A57278	fibrillin-2 precur

ALIGNMENTS

RESULT 1
JE0082
GPI-linked receptor precursor - mouse
N;Alternate names: GFRalpha-3
C;Species: Mus musculus (house mouse)
C;Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: JE0082
R;Nomoto, S.; Ito, S.; Yang, L.X.; Kiuchi, K.
Biochem. Biophys. Res. Commun. 244, 849-853, 1998
A;Title: Molecular cloning and expression analysis of GFRalpha-3,a novel cDNA related to
A;Reference number: JE0082; MUID:98205811; PMID:9535755
A;Accession: JE0082
A;Molecule type: mRNA
A;Residues: 1-397 <NOM>
A;Cross-references: UNIPROT:O35118; UNIPARC:UPI000002231A; DDBJ:AB008833; NID:g2627159;
C;Comment: This protein plays a distinct role in cell survival and differentiation.
C;Superfamily: Mus musculus GPI-linked receptor
C;Keywords: glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;380-397/Region: hydrophobic
F;92,145,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 2131; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 8.2e-166;
Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
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Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
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Db        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240

Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300

Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
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Db        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
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Db        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397

RESULT 2
S02392
alpha-2-macroglobulin receptor precursor - human
N;Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptc
C;Species: Homo sapiens (man)
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C;Accession: S02392; S30027; I37998; A39210; S12538
R;Herz, J.; Hamann, U.; Rogne, S.; Myklebost, O.; Gausepohl, H.; Stanley, K.K.
EMBO J. 7, 4119-4127, 1988
A;Title: Surface location and high affinity for calcium of a 500-kd liver membrane prote
A;Reference number: S02392; MUID:89210795; PMID:3266596
A;Accession: S02392
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-4544 <HER>
A;Cross-references: UNIPROT:Q07954; UNIPARC:UPI0000055B03; EMBL:X13916; NID:g34338; PIDN
R;Kristensen, T.
submitted to the EMBL Data Library, October 1990
A;Reference number: S30027
A;Accession: S30027
A;Molecule type: mRNA
A;Residues: 3275-3864 <KRI>
A;Cross-references: UNIPARC:UPI00001736CD; EMBL:X55077
R;Herz, J.; Kowal, R.C.; Goldstein, J.L.; Brown, M.S.
EMBO J. 9, 1769-1776, 1990
A;Title: Proteolytic processing of the 600 kd low density lipoprotein receptor-related p
A;Reference number: S12538; MUID:90269210; PMID:2112085
A;Contents: annotation; site of proteolytic cleavage
R;Kutt, H.; Herz, J.; Stanley, K.K.
Biochim. Biophys. Acta 1009, 229-236, 1989
A;Title: Structure of the low-density lipoprotein receptor-related protein (LRP) promote
A;Reference number: I37998; MUID:90089395; PMID:2597675
A;Accession: I37998
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <RES>
A;Cross-references: UNIPARC:UPI0000000A1E; EMBL:X15424; NID:g34408; PIDN:CAA33464.1; PID
R;Strickland, D.K.; Ashcom, J.D.; Williams, S.; Burgess, W.H.; Migliorini, M.; Argraves,
J. Biol. Chem. 265, 17401-17404, 1990
A;Title: Sequence identity between the alpha2-macroglobulin receptor and low density lip
A;Reference number: A39210; MUID:91009181; PMID:1698775
A;Accession: A39210
A;Status: preliminary
A;Molecule type: protein
A;Residues: 150-166;234-238,'X',240-245,'X',247-252;'G',686-695;902-916;1096-1109;'S',17
A;Cross-references: UNIPARC:UPI00001736CE; UNIPARC:UPI00001736CF; UNIPARC:UPI00001736D0;
6D5; UNIPARC:UPI00001736D6; UNIPARC:UPI00001736D7
C;Genetics:
A;Gene: GDB:LRP1; APR; LRP; A2MR
A;Cross-references: GDB:119694; OMIM:107770
A;Map position: 12q13.1-12q13.3
C;Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associat
ciated protein (see PIR:A39875).
C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
C;Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycoprc
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F;198-239/Domain: LDL receptor YWTD-containing repeat homology <YW01>
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F;292-334/Domain: LDL receptor YWTD-containing repeat homology <YW03>
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F;478-519/Domain: EGF homology <EG3>
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F;807-842/Domain: EGF homology <EG4>
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F;976-1011/Domain: LDL receptor ligand-binding repeat homology <LDL6>
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F;3741-3776/Domain: LDL receptor ligand-binding repeat homology <LDLV>
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F;3828-3860/Domain: EGF homology <EG15>
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F;3912-3969/Domain: LDL receptor YWTD-containing repeat homology <YW41>
F;3944-4544/Product: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>
F;3944-4420/Domain: 85K chain extracellular #status predicted <EXT>
F;3970-4012/Domain: LDL receptor YWTD-containing repeat homology <YW42>
F;4013-4056/Domain: LDL receptor YWTD-containing repeat homology <YW43>
F;4057-4099/Domain: LDL receptor YWTD-containing repeat homology <YW44>
F;4100-4142/Domain: LDL receptor YWTD-containing repeat homology <YW45>
F;4151-4182/Domain: EGF homology <EG16>
F;4200-4231/Domain: EGF homology <EG17>
F;4236-4267/Domain: EGF homology <EG18>
F;4272-4303/Domain: EGF homology <EG19>
F;4308-4339/Domain: EGF homology <EG20>
F;4344-4374/Domain: EGF homology <EG21>
F;4377-4408/Domain: EGF homology <EG22>
F;4421-4444/Domain: transmembrane #status predicted <TMM>
F;4445-4544/Domain: intracellular #status predicted <INT>
F;166,2998/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;2958/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;4075,4125,4278/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             6.2%;  Score 132;  DB 1;  Length 4544;
  Best Local Similarity   20.2%;  Pred. No. 0.043;
  Matches   78;  Conservative   35;  Mismatches  142;  Indels  132;  Gaps   20;

Qy         62 GSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRM----------KHQATCL 111
              |:|  : ||           || :|:::: | |  ||  : |:          :  : |
Db       2615 GTCIGNSSR------CNQFVDCEDASDEM-NCSATDCSSYFRLGVKGVLFQPCERTSLCY 2667

Qy        112 DIYWTVHPARSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDK 171
                 |    |  ||       | |       |     ||      |  |:  :  |   |
Db       2668 APSWVCDGANDCGD-------YSDERDCPGVKRPRCPLNYFACPSGRCIPMSWTCDKEDD 2720

Qy        172 CDRLRKAYGE-------ACS--GIRCQRHLCLAQ---------LRSFFEKAAESHAQG-- 211
              |:     :||        ||      || | |:::             ::||  | :|
Db       2721 CE-----HGEDETHCNKFCSEAQFECQNHRCISKQWLCDGSDDCGDGSDEAA--HCEGKT 2773

Qy        212 ----LLLCP----CAPE------DAGCGERRRNTIAPSCALPSVTPN---------CLDL 248
                  ||    | ||      |  | :    :|| |   |   :          |:
Db       2774 CGPSSFSCPGTHVCVPERWLCDGDKDCADGADESIAAGCLYNSTCDDREFMCQNRQCIPK 2833

Qy        249 RSFCRAD---------------PLC---------------RSRLMDFQTHCHPMDILGT- 277
                 |  |               | |               |    | :  ||
Db       2834 HFVCDHDRDCADGSDESPECEYPTCGPSEFRCANGRCLSSRQWECDGENDCHDQSDEAPK 2893

Qy        278 ---CATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDEC--EQLERSF 332
                  | : : :|          :  |:       || :  | |    ||:|    ||
Db       2894 NPHCTSPEHKC----------NASSQFLCSSGRCVAEALLCNG----QDDCGDSSDERGC 2939

Qy        333 SQNPCLVEAIAAKMRFHRQLFSQDWAD 359
                | ||   ::          |||  |
Db       2940 HINECLSRKLSG--------CSQDCED 2958


RESULT 3
S25111
alpha-2-macroglobulin receptor precursor - mouse
N;Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein recepto
C;Species: Mus musculus (house mouse)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C;Accession: S25111; S32554
R;van Leuven, F.
submitted to the EMBL Data Library, July 1992
A;Reference number: S25111
A;Accession: S25111
A;Molecule type: mRNA
A;Residues: 1-4545 <VAN1>
A;Cross-references: UNIPROT:Q61291; UNIPARC:UPI000002A14E; EMBL:X67469; NID:g49941; PIDN
R;van Leuven, F.; Stas, L.; Raymakers, L.; Overbergh, L.; de Strooper, B.; Hilliker, C.;
Biochim. Biophys. Acta 1173, 71-74, 1993
A;Title: Molecular cloning and sequencing of the murine alpha-2-macroglobulin receptor c
A;Reference number: S32554; MUID:93250049; PMID:8485155
A;Accession: S32554
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-28;4416-4453 <VAN2>
A;Cross-references: UNIPARC:UPI00001736D8; UNIPARC:UPI00001736D9; EMBL:X67469
C;Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associat
ciated protein (see PIR:JX0281).
C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
C;Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycopro
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-3944,3945-4545/Product: alpha-2-macroglobulin receptor #status predicted <MAT>
F;20-3944/Domain: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>
F;28-65/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;73-109/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;116-149/Domain: EGF homology <EG1>
F;155-189/Domain: EGF homology <EG2>
F;199-240/Domain: LDL receptor YWTD-containing repeat homology <YW01>
F;241-282/Domain: LDL receptor YWTD-containing repeat homology <YW02>
F;293-335/Domain: LDL receptor YWTD-containing repeat homology <YW03>
F;336-379/Domain: LDL receptor YWTD-containing repeat homology <YW04>
F;380-421/Domain: LDL receptor YWTD-containing repeat homology <YW05>
F;422-469/Domain: LDL receptor YWTD-containing repeat homology <YW06>
F;479-520/Domain: EGF homology <EG3>
F;572-614/Domain: LDL receptor YWTD-containing repeat homology <YW07>
F;615-660/Domain: LDL receptor YWTD-containing repeat homology <YW08>
F;661-711/Domain: LDL receptor YWTD-containing repeat homology <YW09>
F;712-753/Domain: LDL receptor YWTD-containing repeat homology <YW10>
F;754-800/Domain: LDL receptor YWTD-containing repeat homology <YW11>
F;808-843/Domain: EGF homology <EG4>
F;855-891/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;896-932/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;937-972/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;977-1012/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;1016-1052/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;1063-1098/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F;1105-1141/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F;1146-1183/Domain: LDL receptor ligand-binding repeat homology <LDLA>
F;1186-1222/Domain: EGF homology <EG5>
F;1228-1262/Domain: EGF homology <EG6>
F;1270-1309/Domain: LDL receptor YWTD-containing repeat homology <YW12>
F;1310-1356/Domain: LDL receptor YWTD-containing repeat homology <YW13>
F;1357-1399/Domain: LDL receptor YWTD-containing repeat homology <YW14>
F;1400-1446/Domain: LDL receptor YWTD-containing repeat homology <YW15>
F;1447-1489/Domain: LDL receptor YWTD-containing repeat homology <YW16>
F;1490-1532/Domain: LDL receptor YWTD-containing repeat homology <YW17>
F;1541-1579/Domain: EGF homology <EG7>
F;1584-1627/Domain: LDL receptor YWTD-containing repeat homology <YW18>
F;1628-1670/Domain: LDL receptor YWTD-containing repeat homology <YW19>
F;1671-1714/Domain: LDL receptor YWTD-containing repeat homology <YW20>
F;1715-1754/Domain: LDL receptor YWTD-containing repeat homology <YW21>
F;1755-1797/Domain: LDL receptor YWTD-containing repeat homology <YW22>
F;1798-1847/Domain: LDL receptor YWTD-containing repeat homology <YW23>
F;1851-1887/Domain: EGF homology <EG8>
F;1935-1977/Domain: LDL receptor YWTD-containing repeat homology <YW24>
F;1978-2020/Domain: LDL receptor YWTD-containing repeat homology <YW25>
F;2021-2064/Domain: LDL receptor YWTD-containing repeat homology <YW26>
F;2065-2106/Domain: LDL receptor YWTD-containing repeat homology <YW27>
F;2107-2152/Domain: LDL receptor YWTD-containing repeat homology <YW28>
F;2160-2195/Domain: EGF homology <EG9>
F;2200-2242/Domain: LDL receptor YWTD-containing repeat homology <YW29>
F;2254-2295/Domain: LDL receptor YWTD-containing repeat homology <YW30>
F;2345-2389/Domain: LDL receptor YWTD-containing repeat homology <YW31>
F;2390-2430/Domain: LDL receptor YWTD-containing repeat homology <YW32>
F;2431-2474/Domain: LDL receptor YWTD-containing repeat homology <YW33>
F;2483-2518/Domain: EGF homology <EG10>
F;2525-2562/Domain: LDL receptor ligand-binding repeat homology <LDLB>
F;2567-2601/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F;2606-2640/Domain: LDL receptor ligand-binding repeat homology <LDLD>
F;2653-2689/Domain: LDL receptor ligand-binding repeat homology <LDLE>
F;2697-2731/Domain: LDL receptor ligand-binding repeat homology <LDLF>
F;2735-2770/Domain: LDL receptor ligand-binding repeat homology <LDLG>
F;2775-2813/Domain: LDL receptor ligand-binding repeat homology <LDLH>
F;2819-2854/Domain: LDL receptor ligand-binding repeat homology <LDLI>
F;2859-2898/Domain: LDL receptor ligand-binding repeat homology <LDLJ>
F;2905-2940/Domain: LDL receptor ligand-binding repeat homology <LDLK>
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F;2945-2981/Domain: EGF homology <EG11>
F;2987-3022/Domain: EGF homology <EG12>
F;3030-3069/Domain: LDL receptor YWTD-containing repeat homology <YW34>
F;3070-3114/Domain: LDL receptor YWTD-containing repeat homology <YW35>
F;3115-3157/Domain: LDL receptor YWTD-containing repeat homology <YW36>
F;3158-3201/Domain: LDL receptor YWTD-containing repeat homology <YW37>
F;3202-3242/Domain: LDL receptor YWTD-containing repeat homology <YW38>
F;3243-3285/Domain: LDL receptor YWTD-containing repeat homology <YW39>
F;3295-3331/Domain: EGF homology <EG13>
F;3335-3370/Domain: LDL receptor ligand-binding repeat homology <LDLL>
F;3375-3409/Domain: LDL receptor ligand-binding repeat homology <LDLM>
F;3414-3449/Domain: LDL receptor ligand-binding repeat homology <LDLN>
F;3454-3490/Domain: LDL receptor ligand-binding repeat homology <LDLO>
F;3495-3532/Domain: LDL receptor ligand-binding repeat homology <LDLP>
F;3537-3571/Domain: LDL receptor ligand-binding repeat homology <LDLQ>
F;3576-3610/Domain: LDL receptor ligand-binding repeat homology <LDLR>
F;3614-3648/Domain: LDL receptor ligand-binding repeat homology <LDLS>
F;3655-3691/Domain: LDL receptor ligand-binding repeat homology <LDLT>
F;3696-3732/Domain: LDL receptor ligand-binding repeat homology <LDLU>
F;3742-3777/Domain: LDL receptor ligand-binding repeat homology <LDLV>
F;3786-3823/Domain: EGF homology <EG14>
F;3829-3861/Domain: EGF homology <EG15>
F;3869-3912/Domain: LDL receptor YWTD-containing repeat homology <YW40>
F;3913-3970/Domain: LDL receptor YWTD-containing repeat homology <YW41>
F;3945-4545/Domain: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>
F;3945-4421/Domain: 85K chain extracellular #status predicted <EXT>
F;3971-4013/Domain: LDL receptor YWTD-containing repeat homology <YW42>
F;4014-4057/Domain: LDL receptor YWTD-containing repeat homology <YW43>
F;4058-4100/Domain: LDL receptor YWTD-containing repeat homology <YW44>
F;4101-4143/Domain: LDL receptor YWTD-containing repeat homology <YW45>
F;4152-4183/Domain: EGF homology <EG16>
F;4201-4232/Domain: EGF homology <EG17>
F;4237-4268/Domain: EGF homology <EG18>
F;4273-4304/Domain: EGF homology <EG19>
F;4309-4340/Domain: EGF homology <EG20>
F;4345-4375/Domain: EGF homology <EG21>
F;4378-4409/Domain: EGF homology <EG22>
F;4422-4445/Domain: transmembrane #status predicted <TMM>
F;4446-4545/Domain: intracellular #status predicted <INT>
F;167,2999/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;2959/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;4076,4126,4279/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.1%; Score 131; DB 1; Length 4545;
Best Local Similarity 19.8%; Pred. No. 0.052;
Matches 78; Conservative 39; Mismatches 131; Indels 146; Gaps 21;

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Qy         62 GSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRM----------KHQATCL 111
              |||  : ||           || :|:::: | |  ||  : |:          :  : |
Db       2616 GSCIGNSSR------CNQFVDCEDASDEM-NCSATDCSSYFRLGVKGVLFQPCERTSLCY 2668

Qy        112 DIYWTVHPARSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDK 171
                |    |   ||       | |       |      ||     |  |:  :  |   |
Db       2669 APSWVCDGANDCGD-------YSDERDCPGVKRPRCPLNYFACPSGRCIPMSWTCDKEDD 2721

Qy        172 CDRLRKAYGE-------ACS--GIRCQRHLCLAQ---------LRSFFEKAAESHAQG-- 211
               |:     ||      ||     || | |:::           ::||  | :|
Db       2722 CEN-----GEDETHCNKFCSEAQFECQNHRCISKQWLCDGSDDCGDGSDEAA--HCEGKT 2774

Qy        212 ----LLLCP----CAPE-----------------------DAGCGERR---RNTI---- 232
                  ||    | ||                       :: | :|    :| :
Db       2775 CGPSSFSCPGTHVCVPERWLCDGDKDCTDGADESVTAGCLYNSTCDDREFMCQNRLCIPK 2834

Qy        233 ---------------APSCALPSVTPN--------CLDLRSF-CRADPLCRSRLMDFQT 267
                           :| |  |:  ||         ||  | : |  :  |      :
Db       2835 HFVCDHDRDCADGSDESPECEYPTCGPNEFRCANGRCLSSRQWECDGENDCHDHSDEAPK 2894

Qy        268 HCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDEC-- 325
              : |      | : : :|           :  |:       || :  | |    ||:|
Db       2895 NPH-------CTSPEHKC----------NASSQFLCSSGRCVAEALLCNG----QDDCGD 2933

Qy        326 EQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWAD 359
                 ||    | ||   ::          |||  |
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Db 2934 GSDERGCHVNECLSRKLSG--------CSQDCED 2959

RESULT 4
E89753
protein F11C7.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E89753
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleg
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: E89753
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1722 <STO>
A;Cross-references: UNIPROT:Q19350; UNIPARC:UPI0000074975; GB:chr_X; PIDN:AAC69012.1; PID
C;Genetics:
A;Gene: F11C7.4
A;Map position: X

Query Match 5.8%; Score 124; DB 2; Length 1722;
Best Local Similarity 19.9%; Pred. No. 0.071;
Matches 75; Conservative 53; Mismatches 156; Indels 92; Gaps 21;

```
Qy         34 ENRFVNSCTQ---ARKKC---EANPACKAAYQHLGS-CTSSLSRPLPLEESAMSADCLEA 86
              | | || |       | |    : |||:    : |  |   |:     : |: :     |
Db       1327 EQRDVNECNHYDCNRGHCVMTVSGPACQCEMGYTGRFCEKLLN-----QCSSNTCSSRGA 1381

Qy         87 AEQLRNSSLIDC-------RCHRRMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTS 139
                 : |::: :|         |  :|    ||||       |  : |
Db       1382 CSPVWNNTVCNCDNNWRGAHCQHQMD---TCLDF-----PCNNDG--------------- 1418

Qy        140 KPWKMNLSKLNMLKPDSDLCLKFAM--LCTLHDKCDRLRKAYGEACSGIRCQRHLCLAQL 197
                 : : |      |  | || |   | :   | : :  :|| |  :  : | |   :
Db       1419 ------VCRTNDENTFSCECQKFFMGTRCEIEGSCLKAQCVHGE-CIQLSPETHTCSCNI 1471

Qy        198 RSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNC---LD--LRSFC 252
               :  | :          ||    | | | :      :||:     :|   :|    ||
Db       1472 -GYEGDACDKKIDYCKAGPCL-NGANC-ENKLTGYKCTCAVGFEGADCEINIDECALEFC 1528

Qy        253 RADPLCRSRLMDFQTHCHPMDILG-TCATEQSRCLRAYLGLIGTAMTPNFISK--VNTTV 309
              :    || :: |::  |       |  | |: : |          |   | |:    ||
Db       1529 KNGAKCRDKINDYECVCDGTGFEGRNCTTDINEC----------ANPNNCINGECTNTLG 1578

Qy        310 ALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQQN 369
                 | || :| :   |          :|||  :  :  :                |: : | :
Db       1579 NYKCACR-NGFIGPRCS------VRNPCTAQIASNNI-------------SSVTCVHGKC 1618

Qy        370 SNPALRLQPRLPILSF 385
               || ::::    :  :
Db       1619 VNPVVQIEKNREVAKY 1634
```

RESULT 5
T09059
notch4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09059
R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sch
submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: Z16543
A;Accession: T09059
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1964 <ROW>
A;Cross-references: UNIPROT:P31695; UNIPARC:UPI000016C7F1; EMBL:AF030001; NID:g2564945; P
C;Genetics:

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: March 7, 2006, 23:29:32 ; Search time 56.979 Seconds
(without alignments)
4915.754 Million cell updates/sec

Title: US-10-621-855-5
Perfect score: 2131
Sequence: 1 MGLSWSPRPPLLMILLLVLS.....PRLPILSFSILPLILLQTLW 397

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2131	100.0	397	1	GFRA3_MOUSE	O35118 mus musculu
2	2058	96.6	385	2	Q9R2D0_MOUSE	Q9r2d0 mus musculu
3	1972	92.5	397	2	Q6AXR3_RAT	Q6axr3 rattus norv
4	1646.5	77.3	400	1	GFRA3_HUMAN	O60609 homo sapien
5	1167	54.8	222	2	Q9QZG2_RAT	Q9qzg2 rattus norv
6	581.5	27.3	465	1	GFRA2_CHICK	O13157 gallus gall
7	577.5	27.1	444	2	Q792X9_RAT	Q792x9 rattus norv
8	577.5	27.1	464	2	Q5E9X0_BOVIN	Q5e9x0 bos taurus
9	577.5	27.1	464	2	O35977_RAT	O35977 rattus norv
10	576.5	27.1	463	1	GFRA2_MOUSE	O08842 mus musculu
11	576.5	27.1	463	2	Q920Y3_MOUSE	Q920y3 mus musculu
12	574.5	27.0	460	2	Q5RE29_PONPY	Q5re29 pongo pygma
13	574.5	27.0	464	1	GFRA2_HUMAN	O00451 homo sapien
14	574.5	27.0	464	2	Q6GTR9_HUMAN	Q6gtr9 homo sapien
15	574.5	27.0	464	2	Q5RAD6_PONPY	Q5rad6 pongo pygma
16	564.5	26.5	464	2	Q5R9T3_PONPY	Q5r9t3 pongo pygma
17	531	24.9	469	1	GFRA1_CHICK	O13156 gallus gall
18	519	24.4	495	2	Q6T5C3_BRARE	Q6t5c3 brachydanio
19	514.5	24.1	481	2	Q98TT8_BRARE	Q98tt8 brachydanio
20	513.5	24.1	465	1	GFRA1_HUMAN	P56159 homo sapien
21	513	24.1	472	2	Q98TT9_BRARE	Q98tt9 brachydanio
22	510	23.9	463	2	O35252_MOUSE	O35252 mus musculu
23	508.5	23.9	468	1	GFRA1_MOUSE	P97785 mus musculu
24	508.5	23.9	468	2	O35246_MOUSE	O35246 mus musculu
25	507	23.8	431	2	Q4RG68_TETNG	Q4rg68 tetraodon n
26	507	23.8	463	2	O35748_RAT	O35748 rattus norv
27	505.5	23.7	468	1	GFRA1_RAT	Q62997 rattus norv
28	490	23.0	431	1	GFRA4_CHICK	O93512 gallus gall
29	489.5	23.0	484	2	Q4S1R4_TETNG	Q4s1r4 tetraodon n
30	468.5	22.0	333	2	Q4RTG0_TETNG	Q4rtg0 tetraodon n
31	442.5	20.8	358	2	Q9Z2A3_MOUSE	Q9z2a3 mus musculu
32	436.5	20.5	359	2	Q58J92_HUMAN	Q58j92 homo sapien
33	429.5	20.2	342	2	Q4SDM1_TETNG	Q4sdm1 tetraodon n
34	429	20.1	330	2	Q9Z2A2_MOUSE	Q9z2a2 mus musculu
35	412	19.3	203	2	Q4SFK7_TETNG	Q4sfk7 tetraodon n
36	375.5	17.6	260	1	GFRA4_MOUSE	Q9jjt2 mus musculu
37	371	17.4	273	1	GFRA4_RAT	Q9epi2 rattus norv
38	294	13.8	299	1	GFRA4_HUMAN	Q9gzz7 homo sapien
39	294	13.8	299	2	Q5JT74_HUMAN	Q5jt74 homo sapien
40	272.5	12.8	247	2	Q4SG83_TETNG	Q4sg83 tetraodon n
41	264.5	12.4	182	2	Q5JT77_HUMAN	Q5jt77 homo sapien
42	232	10.9	394	2	Q6UXV0_HUMAN	Q6uxv0 homo sapien
43	223.5	10.5	393	2	Q6SJE0_MOUSE	Q6sje0 mus musculu
44	204	9.6	225	2	Q9QWK2_MOUSE	Q9qwk2 mus musculu
45	199.5	9.4	109	2	Q8JG58_AMBME	Q8jg58 ambystoma m

ALIGNMENTS

RESULT 1
GFRA3_MOUSE
ID GFRA3_MOUSE STANDARD; PRT; 397 AA.
AC O35118; O35325; O55243; Q6NZC2; Q8C8L9;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE GDNF family receptor alpha 3 precursor (GFR-alpha 3) (GFRalpha3).
GN Name=Gfra3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Heart;
RX MEDLINE=98205811; PubMed=9535755; DOI=10.1006/bbrc.1998.8361;
RA Nomoto S., Ito S., Yang L.-X., Kiuchi K.;
RT "Molecular cloning and expression analysis of GFR alpha-3, a novel
RT cDNA related to GDNFR alpha and NTNR-alpha.";
RL Biochem. Biophys. Res. Commun. 244:849-853(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98420233; PubMed=9749804;
RA Widenfalk J., Tomac A., Lindqvist E., Hoffer B., Olson L.;
RT "GFRalpha-3, a protein related to GFRalpha-1, is expressed in
RT developing peripheral neurons and ensheathing cells.";
RL Eur. J. Neurosci. 10:1508-1517(1998).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=9448325; DOI=10.1073/pnas.95.3.1295;
RA Naveilhan P., Baudet C., Mikaels A., Shen L., Westphal H., Ernfors P.;
RT "Expression and regulation of GFRalpha3, a glial cell line-derived
RT neurotrophic factor family receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:1295-1300(1998).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98245162; PubMed=9576965; DOI=10.1073/pnas.95.10.5801;
RA Baloh R.H., Gorodinsky A., Golden J.P., Tansey M.G., Keck C.L.,
RA Popescu N.C., Johnson E.M. Jr., Milbrandt J.;
RT "GFRalpha3 is an orphan member of the GDNF/neurturin/persephin
RT receptor family.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:5801-5806(1998).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98271460; PubMed=9608533; DOI=10.1006/mcne.1998.0667;
RA Trupp M., Raynoschek C., Belluardo N., Ibanez C.F.;
RT "Multiple GPI-anchored receptors control GDNF-dependent and
RT independent activation of the c-Ret receptor tyrosine kinase.";
RL Mol. Cell. Neurosci. 11:47-63(1998).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Adrenal gland;

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RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Receptor for the glial cell line-derived neurotrophic
CC       factor, artemin. Mediates the artemin-induced autophosphorylation
CC       and activation of the RET receptor tyrosine kinase (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the GDNFR family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AB008833; BAA23562.1; -; mRNA.
DR   EMBL; AF041842; AAC23558.1; -; mRNA.
DR   EMBL; AF036163; AAC24468.1; -; mRNA.
DR   EMBL; AF051766; AAC24354.1; -; mRNA.
DR   EMBL; AF020305; AAB70931.1; -; mRNA.
DR   EMBL; AK046542; BAC32778.1; -; mRNA.
DR   EMBL; BC066202; AAH66202.1; -; mRNA.
DR   PIR; JE0082; JE0082.
DR   Ensembl; ENSMUSG00000024366; Mus musculus.
DR   MGI; MGI:1201403; Gfra3.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0008046; F:axon guidance receptor activity; IMP.
DR   GO; GO:0015026; F:coreceptor activity; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0007411; P:axon guidance; IMP.
DR   GO; GO:0007422; P:peripheral nervous system development; IMP.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.
DR   InterPro; IPR003438; GDNF_receptor.
DR   InterPro; IPR003505; GDNF_receptorA3.
DR   PANTHER; PTHR10269; GDNF_receptor; 1.
DR   Pfam; PF02351; GDNF; 1.
DR   PRINTS; PR01319; GDNFRALPHA3.
DR   PRINTS; PR01316; GDNFRECEPTOR.
KW   Glycoprotein; GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
FT   SIGNAL        1     28       Potential.
FT   CHAIN        29    371       GDNF family receptor alpha 3.
FT   PROPEP      372    397       Removed in mature form (Potential).
FT   LIPID       371    371       GPI-anchor amidated asparagine
FT                                (Potential).
FT   CARBOHYD     92     92       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    145    145       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    306    306       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT      5      6       WS -> LE (in Ref. 2 and 3).
FT   CONFLICT     66     66       S -> C (in Ref. 6).
FT   CONFLICT    218    218       A -> P (in Ref. 2, 3 and 5).
FT   CONFLICT    314    314       T -> S (in Ref. 7).
SQ   SEQUENCE   397 AA;  44307 MW;  BB66CEF65D32A4B9 CRC64;

  Query Match             100.0%;  Score 2131;  DB 1;  Length 397;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-171;
  Matches  397;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240

Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300

Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360

Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
              |||||||||||||||||||||||||||||||||||||
Db        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397


RESULT 2
Q9R2D0_MOUSE
ID   Q9R2D0_MOUSE PRELIMINARY;      PRT;   385 AA.
AC   Q9R2D0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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DE   TGF-beta-related neurotrophic receptor-3 precursor.
GN   Name=Gfra3; Synonyms=TrnR-3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Swiss-Webster /NIH; TISSUE=Embryo;
RA   Zhong J., Annies M., Tolle A., Heumann R.;
RT   "Molecular cloning of a new member of TrnR family.";
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Y15110; CAA75384.1; -; mRNA.
DR   MGI; MGI:1201403; Gfra3.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0008046; F:axon guidance receptor activity; IMP.
DR   GO; GO:0015026; F:coreceptor activity; TAS.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0007411; P:axon guidance; IMP.
DR   GO; GO:0007422; P:peripheral nervous system development; IMP.
DR   GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; TAS.
DR   InterPro; IPR003438; GDNF_receptor.
DR   InterPro; IPR003505; GDNF_receptorA3.
DR   Pfam; PF02351; GDNF; 1.
DR   PRINTS; PR01319; GDNFRALPHA3.
DR   PRINTS; PR01316; GDNFRECEPTOR.
KW   Receptor; Signal.
FT   SIGNAL       1     15       Potential.
SQ   SEQUENCE   385 AA;  42997 MW;  91A7F3F9FF30ED14 CRC64;

  Query Match             96.6%;  Score 2058;  DB 2;  Length 385;
  Best Local Similarity   99.7%;  Pred. No. 5.2e-165;
  Matches  384;  Conservative    0;  Mismatches   1;  Indels    0;  Gaps    0;

Qy         13 MILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCTSSLSRPL 72
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCTSSLSRPL 60

Qy         73 PLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYELDVSP 132
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGDYELDVSP 120

Qy        133 YEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIRCQRHL 192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIRCQRHL 180

Qy        193 CLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLDLRSFC 252
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        181 CLAQLRSFFEKAAESHAQGLLLCPCPPEDAGCGERRRNTIAPSCALPSVTPNCLDLRSFC 240

Qy        253 RADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALS 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALS 300

Qy        313 CTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQQNSNP 372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQQNSNP 360

Qy        373 ALRLQPRLPILSFSILPLILLQTLW 397
              |||||||||||||||||||||||||
Db        361 ALRLQPRLPILSFSILPLILLQTLW 385


RESULT 3
Q6AXR3_RAT
ID   Q6AXR3_RAT  PRELIMINARY;      PRT;   397 AA.
AC   Q6AXR3;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Glial cell line derived neurotrophic factor family receptor alpha
DE   3.
GN   Name=Gfra3;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RG   NIH MGC Project;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC079378; AAH79378.1; -; mRNA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003438; GDNF_receptor.
DR   InterPro; IPR003505; GDNF_receptorA3.
DR   Pfam; PF02351; GDNF; 1.
DR   PRINTS; PR01319; GDNFRALPHA3.
DR   PRINTS; PR01316; GDNFRECEPTOR.
KW   Receptor.
SQ   SEQUENCE   397 AA;  44053 MW;  E11D2E7B9CB46AF8 CRC64;

  Query Match             92.5%;  Score 1972;  DB 2;  Length 397;
  Best Local Similarity   92.9%;  Pred. No. 9.6e-158;
  Matches  369;  Conservative    9;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          1 MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQH 60
              |||| ||||| |:||||||||||||| |||| |||| ||||||||||||||||||||||
Db          1 MGLSRSPRPPPLVILLLVLSLWLPLGTGNSLPTENRLVNSCTQARKKCEANPACKAAYQH 60

Qy         61 LGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPA 120
              | ||| ||| ||| ||| || |||||:||||||||||||||||||||||||||||||||
Db         61 LDSCTPSLSSPLPSGESATSAACLEAAQQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPV 120

Qy        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYG 180
              ||||||||||||||||||||||||||||||:||||||||||||||||||:||||||||||
Db        121 RSLGDYELDVSPYEDTVTSKPWKMNLSKLSMLKPDSDLCLKFAMLCTLNDKCDRLRKAYG 180

Qy        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 EACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPS 240

Qy        241 VTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VAPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPN 300

Qy        301 FISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADS 360
              |||||||||| |||||||||||:||||||||:||||||||||||||||||||||||||||
Db        301 FISKVNTTVALGCTCRGSGNLQDECEQLEKSFSQNPCLMEAIAAKMRFHRQLFSQDWADS 360
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Qy        361 TFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
              ||||:|||||:|||| | |||:||| || ||||||||
Db        361 TFSVMQQQNSSPALRPQLRLPVLSFFILTLILLQTLW 397


RESULT 4
GFRA3_HUMAN
ID   GFRA3_HUMAN    STANDARD;      PRT;   400 AA.
AC   O60609; Q6UW20; Q8IUZ2;
DT   16-OCT-2001 (Rel. 40, Created)
DT   25-OCT-2004 (Rel. 45, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   GDNF family receptor alpha 3 precursor (GFR-alpha 3) (GFRalpha3).
GN   Name=GFRA3; ORFNames=UNQ339/PRO538/PRO3664;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORM 1), AND TISSUE SPECIFICITY.
RX   MEDLINE=98245162; PubMed=9576965; DOI=10.1073/pnas.95.10.5801;
RA   Baloh R.H., Gorodinsky A., Golden J.P., Tansey M.G., Keck C.L.,
RA   Popescu N.C., Johnson E.M. Jr., Milbrandt J.;
RT   "GFRalpha3 is an orphan member of the GDNF/neurturin/persephin
RT   receptor family.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:5801-5806(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA   Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA   Wood W.I., Godowski P.J., Gray A.M.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   PROTEIN SEQUENCE OF 32-46.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [5]
RP   FUNCTION.
RX   MEDLINE=99098192; PubMed=9883723; DOI=10.1016/S0896-6273(00)80649-2;
RA   Baloh R.H., Tansey M.G., Lampe P.A., Fahrner T.J., Enomoto H.,
RA   Simburger K.S., Leitner M.L., Araki T., Johnson E.M. Jr.,
RA   Milbrandt J.;
RT   "Artemin, a novel member of the GDNF ligand family, supports
RT   peripheral and central neurons and signals through the GFRalpha3-RET
RT   receptor complex.";
RL   Neuron 21:1291-1302(1998).
CC   -!- FUNCTION: Receptor for the glial cell line-derived neurotrophic
CC       factor, artemin. Mediates the artemin-induced autophosphorylation
CC       and activation of the RET receptor tyrosine kinase.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=O60609-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=O60609-2; Sequence=VSP_010942;
CC   -!- TISSUE SPECIFICITY: Widely expressed in adult and fetus which
CC       exhibit a similar pattern. Essentially not expressed in the
CC       central nervous system, but highly expressed in several sensory
CC       and sympathetic ganglia of the peripheral nervous system. Moderate
CC       expression in many nonneuronal tissues, particularly those of the
CC       digestive and urogenital systems, but high expression in stomach
CC       and appendix. Several types of glandular tissues show low
CC       expression. Very low or no expression detected in the
CC       hematopoietic system.
CC   -!- SIMILARITY: Belongs to the GDNFR family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF051767; AAC24355.1; -; mRNA.
DR   EMBL; AY358997; AAQ89356.1; -; mRNA.
DR   EMBL; AY359037; AAQ89396.1; -; mRNA.
DR   EMBL; BC037951; AAH37951.1; -; mRNA.
DR   Ensembl; ENSG00000146013; Homo sapiens.
DR   HGNC; HGNC:4245; GFRA3.
DR   MIM; 605710; -.
DR   GO; GO:0019898; C:extrinsic to membrane; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0007422; P:peripheral nervous system development; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR003438; GDNF_receptor.
DR   InterPro; IPR003505; GDNF_receptorA3.
DR   PANTHER; PTHR10269; GDNF_receptor; 1.
DR   Pfam; PF02351; GDNF; 1.
DR   PRINTS; PR01319; GDNFRALPHA3.
DR   PRINTS; PR01316; GDNFRECEPTOR.
KW   Alternative splicing; Direct protein sequencing; Glycoprotein;
KW   GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
FT   SIGNAL       1    31
FT   CHAIN       32   374       GDNF family receptor alpha 3.
FT   PROPEP     375   400       Removed in mature form (Potential).
FT   LIPID      374   374       GPI-anchor amidated asparagine
FT                              (Potential).
FT   CARBOHYD    95    95       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   148   148       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   309   309       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC   127   157       Missing (in isoform 2).
FT                              /FTId=VSP_010942.
FT   CONFLICT   108   108       K -> R (in Ref. 1).
SQ   SEQUENCE   400 AA;  44511 MW;  B0BC252FE1F072C7 CRC64;

  Query Match             77.3%;  Score 1646.5;  DB 1;  Length 400;
  Best Local Similarity   77.8%;  Pred. No. 2.7e-130;
  Matches  305;  Conservative   30;  Mismatches   56;  Indels    1;  Gaps    1;
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Qy          7 PRPP-LLMILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKAAYQHLGSCT 65
              | ||  :||:|||:     ||| ||: | ||:| :||| |||:||:|:| | ||| || |||
Db          9 PLPPVVLMLLLLLPPSPLPLAAGDPLPTESRLMNSCLQARRKCQADPTCSAAYHHLDSCT 68

Qy         66 SSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIYWTVHPARSLGD 125
              ||:| ||| || :: |||||||:|||||||  | ||||||:|   |||||||| |||||:
Db         69 SSISTPLPSEEPSVPADCLEAAQQLRNSSLIGCMCHRRMKNQVACLDIYWTVHRARSLGN 128

Qy        126 YELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSG 185
              ||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db        129 YELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLNDKCDRLRKAYGEACSG 188

Qy        186 IRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNC 245
              ||||:|| || :||||||| |||||||||||  | |||||||||||:|||| | |||
Db        189 PHCQRHVCLRQLLTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNC 248

Qy        246 LDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKV 305
              |:||  | :||||||||:|||||||||||||||||||||||||||||||||||:| |
Db        249 LELRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFVSNV 308

Qy        306 NTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVV 365
              ||:|||||||||||:||| ||  || |||| |||||||||  |||||||   ||:|:
Db        309 NTSVALSCTCRGSGNLQEECEMLEGFFSHNPCLTEAIAAKMRFHSQLFSQDWPHPTFAVM 368

Qy        366 QQQNSNPALRLQPRLPILSFSILPLILLQTLW 397
                || |||:| ||.:| |    |||||| :||
Db        369 AHQNENPAVRPQPWVPSLFSCTLPLILLLSLW 400


RESULT 5
Q9QZG2_RAT
ID   Q9QZG2_RAT  PRELIMINARY;      PRT;   222 AA.
AC   Q9QZG2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   GDNF-family receptor alpha 3 (Fragment).
GN   Name=Gfra3; Synonyms=GFRalpha-3;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Cochlea;
RX   MEDLINE=20185640; PubMed=10719212; DOI=10.1016/S0169-328X(99)00328-9;
RA   Stover T., Gong T.L., Cho Y., Altschuler R.A., Lomax M.I.;
RT   "Expression of the GDNF family members and their receptors in the
RT   mature rat cochlea.";
RL   Brain Res. Mol. Brain Res. 76:25-35(2000).
DR   EMBL; AF184920; AAF01242.1; -; mRNA.
DR   Ensembl; ENSRNOG00000020309; Rattus norvegicus.
DR   RGD; 620502; Gfra3.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003438; GDNF_receptor.
DR   InterPro; IPR003505; GDNF_receptorA3.
DR   Pfam; PF02351; GDNF; 1.
DR   PRINTS; PR01319; GDNFRALPHA3.
DR   PRINTS; PR01316; GDNFRECEPTOR.
KW   Receptor.
FT   NON_TER     1      1
FT   NON_TER     222    222
SQ   SEQUENCE   222 AA;  24791 MW;  A9610F6462468C74 CRC64;

  Query Match             54.8%;  Score 1167;  DB 2;  Length 222;
  Best Local Similarity   96.4%;  Pred. No. 3.8e-90;
  Matches  214;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        136 TVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKCDRLRKAYGEACSGIRCQRHLCLA 195
              ||||||||||||||:||||||||||||||||:|:|||||||||||||||||||||||||
Db          1 TVTSKPWKMNLSKLSMLKPDSDLCLKFAMLCTLNDRCDRLRKAYGEACSGIRCQRHLCLA 60

Qy        196 QLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVTPNCLDLRSFCRAD 255
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||| |||
Db         61 QLRSFFEKAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCALPSVAPNCLDLRSFRRAD 120

Qy        256 PLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        121 PLCRSRLMDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALGCTC 180

Qy        316 RGSGNLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDW 357
              |||||||||||||:||||||:||||||||||||||||||
Db        181 RGSGNLQDECEQLEKSFSQNPCLMEAIAAKMRFHRQLFSQDW 222


RESULT 6
GFRA2_CHICK
ID   GFRA2_CHICK    STANDARD;      PRT;   465 AA.
AC   O13157;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   GDNF family receptor alpha 2 precursor (GFR-alpha 2) (Neurturin
DE   receptor alpha) (NTNR-alpha) (NRTNR-alpha) (GDNF receptor beta)
DE   (GDNFR-beta).
GN   Name=GFRA2; Synonyms=GDNFRB;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=97336104; PubMed=9192899; DOI=10.1038/42729;
RA   Buj-Bello A., Adu J., Pinon L.G.P., Horton A., Thompson J.,
RA   Rosenthal A., Chinchetru M., Buchman V.L., Davies A.M.;
RT   "Neurturin responsiveness requires a GPI-linked receptor and the Ret
RT   receptor tyrosine kinase.";
RL   Nature 387:721-724(1997).
CC   -!- FUNCTION: Receptor for neurturin. Mediates the NRTN-induced
CC       autophosphorylation and activation of the RET receptor. Also able
CC       to mediate GDNF signaling through the RET tyrosine kinase receptor
CC       (By similarity).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- SIMILARITY: Belongs to the GDNFR family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U90542; AAB61571.1; -; mRNA.
DR   Ensembl; ENSGALG00000001795; Gallus gallus.
DR   InterPro; IPR003438; GDNF_receptor.
DR   InterPro; IPR003504; GDNF_receptorA2.
DR   PANTHER; PTHR10269; GDNF_receptor; 1.
DR   Pfam; PF02351; GDNF; 1.
DR   PRINTS; PR01318; GDNFRALPHA2.
DR   PRINTS; PR01316; GDNFRECEPTOR.
KW   Glycoprotein; GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
FT   SIGNAL      1     21       Potential.
FT   CHAIN       22    445      GDNF family receptor alpha 2.
FT   PROPEP      446   465      Removed in mature form (Potential).
FT   LIPID       445   445      GPI-anchor amidated serine (Potential).
FT   CARBOHYD    355   355      N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    387   387      N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    412   412      N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   465 AA;  51909 MW;  22CD9024ED971F06 CRC64;

  Query Match             27.3%;  Score 581.5;  DB 1;  Length 465;
  Best Local Similarity   36.0%;  Pred. No. 2.1e-40;
  Matches  130;  Conservative   51;  Mismatches  135;  Indels   45;  Gaps   11;
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Qy         41 CTQARKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRC 100
              | :| | | |  :| : |: |  | :   |   |     : :|  | | |: | | ||||
Db         40 CIRANKLCAAEGSCSSRYRTLRQCLAGRDRNTML----ANKECQAALEVLQESPLYDCRC 95

Qy        101 HRRMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSKPWKMNLSKLNML-------- 152
               | |: :  || :||::|   : |:   : ||||  :||:     || :  |
Db         96 KRGMRKEIQCLQVYWSIHLGLAEGEEFYEASPYE-PITSR-----LSDIFRLASIFSGMD 149

Qy        153 ---KPDSDLCLKFAMLCTLHDKCDRLRKAYGEACS-----GIRCQRHLCLAQLRSFFEKA 204
                 |: ||  |  | |:| | |||  |   ||       | |  |   || ||:
Db        150 PATNSKSNHCLDAAKACNLNDNCKRLRSGYISTCSKEISATEHCSRRKCHKALRQFFDNV 209

Qy        205 AESHAQGLLLCPCAPEDAGCGERRRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSRLM 263
              :  || | |  :|  | | || || | |:      |||||||: |||| ||||||
Db        210 PSEYTYRLLFCSC--KDQACAEPRRQTIVPFCSYEDKEKPNCLDLRNVCRADHLCRSRLA 267

Qy        264 DFQTHCH-PMDILGTCATEQ-SRCLRAYLGLIGTAMTPNFISKVNTTVALS--CTCRGSG 319
              ||  :|      | :|  :    || :| |||| ||||::    |:: :|  |:|:|||
Db        268 DFHANCQASFQSLTSCPGDNYQACLGSYTGLIGFDMTPNYVDASTTSITISPWCSCKGSG 327

Qy        320 NLQDECEQLERSFSQNPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQQNSNPALRLQPR 379
              ||::|||:  | |::|||| ||           | : : |  :  :| :| : : |:
Db        328 NLEEECEKFLRDFTENPCLRNAI----------QAFGNGTDVNLSPKNPSPPITMLPK 375

Qy        380 L 380
              :
Db        376 V 376
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RESULT 7
Q792X9_RAT
ID Q792X9_RAT PRELIMINARY; PRT; 444 AA.
AC Q792X9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE GDNF receptor-beta (Fragment).
GN Name=Gfra2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Hippocampus;
RX MEDLINE=97402208; PubMed=9259272; DOI=10.1093/hmg/6.8.1267;
RA Suvanto P., Wartiovaara K., Lindahl M., Arumae U., Moshnyakov M.,
RA Horelli-Kuitunen N., Airaksinen M.S., Palotie A., Sariola H.,
RA Saarma M.;
RT "Cloning, mRNA distribution and chromosomal localisation of the gene
RT for glial cell line-derived neurotrophic factor receptor beta, a
RT homologue to GDNFR-alpha.";
RL Hum. Mol. Genet. 6:1267-1273(1997).
DR EMBL; AF003825; AAD09310.1; -; mRNA.
DR RGD; 61809; Gfra2.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003504; GDNF_receptorA2.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01318; GDNFRALPHA2.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor.
FT NON_TER 444 444
SQ SEQUENCE 444 AA; 49578 MW; A548644EDB36D5F3 CRC64;

Query Match 27.1%; Score 577.5; DB 2; Length 444;
Best Local Similarity 38.8%; Pred. No. 4.3e-40;
Matches 127; Conservative 40; Mismatches 125; Indels 35; Gaps 9;

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Qy         41 CTQARKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRC 100
              | :| : | |   | : |: |  | :   |   |     : :|  | | |: | | ||||
Db         40 CVRANELCAAESNCSSRYRTLRQCLAGRDRNTML----ANKECQAALEVLQESPLYDCRC 95

Qy        101 HRRMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSKPWKMNLSKLNML-------- 152
               | || :  || |||::|   : |:   : ||||  |||:     || :  |
Db         96 KRGMKKELQCLQIYWSIHLGLTEGEEFYEASPYE-PVTSR-----LSDIFRLASIFSGTG 149

Qy        153 -----KPDSDLCLKFAMLCTLHDKCDRLRKAYGEACS-----GIRCQRHLCLAQLRSFFE 202
                    |: ||  |  | |:| | :|| :|   |:        || |  |   || ||:
Db        150 TDPAVSTKSNHCLDAAKACNLNDNCKKLRSSYISICNREISPTERCNRRKCHKALRQFFD 209

Qy        203 KAAESHAQGLLLCPCAPEDAGCGERRRNTIAPSCAL-PSVTPNCLDLRSFCRADPLCRSR 261
              :    :   :| | |  :|  | |||| || |||:      |||||||| || | |||||
Db        210 RVPSEYTYRMLFCSC--QDQACAERRRQTILPSCSYEDKEKPNCLDLRSLCRTDHLCRSR 267

Qy        262 LMDFQTHCHP--MDILGTCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALS--CTCRG 317
              | ||  :|      |    |     || :| |:||  ||||::    | : :|  | |||
Db        268 LADFHANCRASYRTITSCPADNYQACLGSYAGMIGFDMTPNYVDSNPTGIVVSPWCNCRG 327

Qy        318 SGNLQDECEQLERSFSQNPCLVEAIAA 344
              |||:::|||:  | |::||||  || |
Db        328 SGNMEEECEKFLRDFTENPCLRNAIQA 354
```

RESULT 8
Q5E9X0_BOVIN
ID Q5E9X0_BOVIN PRELIMINARY; PRT; 464 AA.
AC Q5E9X0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE GDNF family receptor alpha 2 preproprotein.
GN Name=GFRA2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
RA Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,
RA Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
RA Pertea G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
RA Keele J.W.;
RT "Sequence evaluation of four pooled-tissue normalized bovine cDNA
RT libraries and construction of a gene index for cattle.";
RL Genome Res. 11:626-630(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pooled;
RA Harhay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keele J.W.,
RA Snelling W.M., Weidmann R.T., Smith T.P.L.;
RT "Sequencing and analysis of Bos taurus full-length insert cDNA
RT clones.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BT020800; AAX08817.1; -; mRNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003438; GDNF_receptor.
DR InterPro; IPR003504; GDNF_receptorA2.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01318; GDNFRALPHA2.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor.
SQ SEQUENCE 464 AA; 51658 MW; BF0BF88F4298B5AA CRC64;

Query Match 27.1%; Score 577.5; DB 2; Length 464;
Best Local Similarity 37.9%; Pred. No. 4.6e-40;
Matches 124; Conservative 44; Mismatches 124; Indels 35; Gaps 9;

```
Qy         41 CTQARKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRC 100
              | :| : | |   | : |: |  | :   |   |     : :|  | | |: | | ||||
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